

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Escobedo, Jaime
Quianjin, Hu
Garcia, Pablo
Williams, Lewis T.
Kothakota, Srinivas

(ii) TITLE OF THE INVENTION: Secreted Human Proteins

(iii) NUMBER OF SEQUENCES: 38

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Banner & Witcoff
(B) STREET: 1001 G Street, NW
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20001

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 11-DEC-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/032757
(B) FILING DATE: 11-DEC-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kagan, Sarah A
(B) REGISTRATION NUMBER: 32141
(C) REFERENCE/DOCKET NUMBER: 2441.39505

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-508-9100
(B) TELEFAX: 202-508-9299
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2063 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCTGGCA	CGAGGCCTCA	GTCTTCCAGG	GCGGCGGTGG	GTGTCCGCTT	CTCTCTGCTC	60
TTCGACTGCA	CCGCACTCGC	GCGTGACCCCT	GAATCCCCCT	AGTCAGCTCA	GCGGTGCTGC	120
CATGGCGTGG	CGGCGGCGCG	AAGCCGGCGT	CGGGGCTCGC	GGCGTGTGG	CTCTGGCGTT	180
GCTCGCCCTG	GCCCCTGTGCG	TGCCCGGGGC	CCGGGGCCGG	GCTCTCGAGT	GGTTCTCGGC	240
CGTGGTAAAC	ATCGAGTACG	TGGACCCGCA	GACCAACCTG	ACGGTGTGGA	GCGTCTCGGA	300
GAGTGGCCGC	TTCGGCGACA	GCTCGCCCAA	GGAGGGCGCG	CATGGCCTGG	TGGGCGTCCC	360
GTGGGCGCCC	GGCAGGAGACC	TCGAGGGCTG	CGCGCCCGAC	ACCGCCTTCT	TCGTGCCCGA	420
GCCCGGCGGC	CGAGGGGCCG	CGCCCTGGGT	CGCCCTGGTG	GCTCGTGGGG	GCTGCACCTT	480
CAAGGACAAG	GTGCTGGTGG	CGGCGCGGAG	GAACGCCTCG	GCCGTCGTCC	TCTACAATGA	540
GGAGCGCTAC	GGGAACATCA	CCTTGCCCAT	GTCTCACGCG	GGAAACAGGAA	ATATAGTGGT	600
CATTATGATT	AGCTATCCAA	AAGGAAGAGA	AATTTGGAG	CTGGTGCAAA	AAGGAATTCC	660
AGTAACGATG	ACCATAGGGG	TTGGCACCCG	GCATGTACAG	GAGTTCATCA	GCGGTCAAGTC	720
TGTGGTGT	GTGGCCATTG	CCTTCATCAC	CATGATGATT	ATCTCGTTAG	CCTGGCTAAT	780
ATTTTACTAT	ATACAGCGTT	TCCTATATAC	TGGCTCTCAG	ATTGGAAGTC	AGAGCCATAG	840
AAAAGAAACT	AAGAAAGTTA	TTGCCAGCT	TCTACTTCAT	ACTGTAAAGC	ATGGAGAAAA	900
GGGAATTGAT	GTTGATGCTG	AAAATTGTGC	AGTGTGTATT	GAAAATTCA	AAGTAAAGGA	960
TATTATTAGA	ATTCTGCCAT	GCAAGCATAT	TTTCATAGA	ATATGCATTG	ACCCATGGCT	1020
TTTGGATCAC	CGAACATGTC	CAATGTGAA	ACTTGATGTC	ATCAAAGCCC	TAGGATATTG	1080
GGGAGAGCCT	GGGGATGTAC	AGGAGATGCC	TGCTCCAGAA	TCTCCTCCTG	GAAGGGATCC	1140
AGCTGCAAAT	TTGAGTCTAG	CTTACCAGA	TGATGACGGA	AGTGTGACCA	GCAGTCCACC	1200
ATCAGCCTCC	CCTGCTGAAT	CTGAGCCACA	GTGTGATCCC	AGCTTTAAAG	GAGATGCAGG	1260
AGAAAATACG	GCATTGCTAG	AAGCCGGCAG	GAGTGACTCT	CGGCATGGAG	GACCCATCTC	1320
CTAGCACACG	TGCCCACTGA	AGTGGCACCA	ACAGAAGTTT	GGCTTGAACT	AAAGGACATT	1380
TTATTTTTT	TACTTTAGCA	CATAATTGT	ATATTTGAAA	ATAATGTATA	TTATTTTAC	1440
TATTAGATT	TGATTTGATA	TACAAAGGAC	TAAGATATT	TCTCTTGAA	GAGACTTTTC	1500
GATTAGTCCT	CATATATTTA	TCTACTAAAA	TAGAGTGT	ACCATGAACA	GTGTGTTGCT	1560
TCAGACTATT	ACAAAGACAA	CTGGGGCAGG	TACTCTAATA	AAAGGACAG	GTGGTGTTC	1620
TAAATAATTG	GCTGCTATGG	TTCTGTAAA	ACCAAGTTAAT	TCTATTTTC	AAGGTTTTG	1680
GCAAAGCACA	TCAATGTTAG	ACTAGTTGAA	GTGGAATTGT	ATAATTCAAT	TCGATAATTG	1740
ATCTCATGGG	CTTCCCTGG	AGGAAAGGTT	TTTTTTGTTG	TTTTTTTTT	AAGAACTTGA	1800
AACTGTAAA	CTGAGATGTC	TGTAGCTTT	TTGCCCATCT	GTAGTGTATG	TGAAGATTTC	1860
AAAACCTGAG	AGCACTTTT	CTTGTGTTAG	AATTATGAGA	AAGGCACCTAG	ATGACTTTAG	1920
GATTGCTATT	TTTCCCTTTA	TTGCCCTCATT	TCTTGTGACG	CCTTGTGTTGGG	GAGGGAAATC	1980
TGTTTATTTT	TTCCCTACAAA	TAAAAAGCTA	AGATTCTATA	TCGCAAAAAAA	AAAAAAAAAA	2040
	AAAAAA	TTCCCTGCGGC	CGC			2063

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCTGGCA	CGAGGTAGGC	AAGGGATAAA	AAGGCACCTA	AGGCCCTTTT	GCAATAAGAA	60
GCCAGATGGA	TAAAGGAAGT	GCTGGTCACC	CTGGAGGTGT	ACTGGTTGGG	GGAAGGTCCC	120

CGGCCCCCAC	AGCCCTCTGG	GGAGCCTCAC	CCTGGCTCTC	CCCACTCACC	TCAGCCCTCA	180
GGCAGCCCC	CCACAGGGCC	CCTCTCCTGC	CTGGACAGCT	CTGCTGGTCT	CCCCGTCCCC	240
TGGAGAAGAA	CAAGGCCATG	GGTCGGCCCC	TGCTGCTGCC	CCTGCTGCTC	CTGCTGCAGC	300
CGCCAGCATT	TCTGCAGCCT	GGTGGCTCCA	CAGGATCTGG	TCCAAGCTAC	CTTTATGGGG	360
TCACTCAACC	AAAACACCTC	TCAGCCTCCA	TGGGTGGCTC	TGTGGAAATC	CCCTTCTCCT	420
TCTATTACCC	CTGGGAGTTA	GCCATAGTTC	CCAACGTGAG	AATATCCTGG	AGACGGGCC	480
ACTTCCACGG	GCAGTCCTTC	TACAGCACAA	GGCCGCCCTTC	CATTACAAG	GATTATGTGA	540
ACCGGGCTTT	TCTGAACTGG	ACAGAGGGTC	AGGAGAGCGG	CTTCCTCAGG	ATCTCAAACC	600
TGCGGAAGGA	GGACCAAGTCT	GTGTATTTCT	GCCGAGTCGA	GCTGGACACC	CGGAGATCAG	660
GGAGGCAGCA	GTTGCAGTCC	ATCAAGGGGA	CCAAACTCAC	CATCACCCAG	GCTGTACAA	720
CCACCACAC	CTGGAGGCC	AGCAGCACAA	CCACCATAGC	CGGCTCAGG	GTCACAGAAA	780
GCAAAGGGCA	CTCAGAACATCA	TGGCACCTAA	GTCTGGACAC	TGCCATCAGG	GTTGCATTGG	840
CTGTCGCTGT	GCTCAAAACT	GTCACTTTGG	GACTGCTGTG	CCTCCTCCTC	CTGTGGTGG	900
GGAGAAGGAA	AGGTAGCAGG	GCGCCAAGCA	GTGACTTCTG	ACCAACAGAG	TGTGGGAGA	960
AGGGATGTGT	ATTAGCCCCG	GAGGACGTGA	TGTGAGACCC	GCTTGTGAGT	CCTCCACACT	1020
CGTTCCCCAT	TGGCAAGATA	CATGGAGAGC	ACCCCTGAGGA	CCTTTAAAAG	GCAAAGCCGC	1080
AAGGCAGAAG	GAGGCTGGGT	CCCTGAATCA	CCGACTGGAG	GAGAGTTACC	TACAAGAGCC	1140
TTCATCCAGG	AGCATCCACA	CTGCAATGAT	ATAGGAATGA	GGTCTGAACT	CCACTGAATT	1200
AAACCACTGG	CATTTGGGGG	CTGTTTATTA	TAGCAGTGCA	AAGAGTTCT	TTATCCTCCC	1260
CAAGGATGGA	AAAATACAAAT	TTATTTTGCT	TACCATAAAA	AAAAAAAAAA	AAAATTCCT	1320
	CGGGCCGC					1328

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCCGGCA	CGAGGGCAAG	ATTCGATACA	AAACCAATGA	ACCTGTGTGG	GAGGAAAAC	60
TCACTTCTT	CATTACAAT	CCCAAGCGCC	AGGACCTTGA	AGTTGAGGTC	AGAGACGAGC	120
AGCACCCAGTG	TTCCCTGGGG	AACTCTGAAGG	TCCCCCTCAG	CCAGCTGCTC	ACCAGTGAGG	180
ACATGACTGT	GAGCCAGCGC	TTCCAGCTCA	GTAACTCGGG	TCCAAACAGC	ACCATCAAGA	240
TGAAGATTGC	CCTGCGGGTG	CTCCATCTCG	AAAAGCGAGA	AAGGCCTCCA	GACCACCAAC	300
ACTCAGCTCA	AGTCAAACGT	CCCTCTGTGT	CCAAAGAGGG	GAGGAAAACA	TCCATCAAAT	360
CTCATATGTC	TGGGTCTCCA	GGCCCTGGGT	GCAGCAACAC	AGCTCCATCC	ACACCAGTCA	420
TTGGGGGCAG	TGATAAACCT	GGTATGGAAG	AAAAGGCCA	GCCCCCTGAG	GCCGGCCCTC	480
AGGGCTGCA	CGACCTGGGC	AGAACCTCCT	CCAGCCTCCT	GGCCTCCCCA	GGCCACATCT	540
CAGTCAGGAA	GCCGACCCCC	AGCATCGCT	CGGACATCTC	GCTGCCCATC	GCCACCCAGG	600
AGCTCGGGCA	AAGGCTGAGG	CAGCTGGAAA	ACGGGACGAC	CCTGGGACAG	TCTCCACTGG	660
GGCAGATCCA	GCTGACCAC	CGGCACAGCT	CGCAGAGAAA	CAAGCTTATC	GTGGTCTGTG	720
ATGCCTGCA	AAACCTCATT	GCCTCTCTG	AAGACGGCTC	TGACCCCTAT	GTCCGCATGT	780
ATTATTACCA	AGACAAGAGG	CGGTCAAGGAA	GGAGGAAAAC	ACACGTGTCA	AAGAAAACAT	840
TAAATCCAGT	GTTTGATCAA	AGCTTTGATT	TCAGTGTTC	GTTACCAAGAA	GTGCAGAGGA	900
GAACGCTCGA	CGTTGCCGTG	AAAGAACAGTG	GCGGCTTCCT	GTCCAAAGAC	AAAGGGCTCC	960
TTGGCAAAGT	ATTGGTTGCT	CTGGCATCTG	AAGAACATTG	CAAAGGCTGG	ACCCAGTGGT	1020
ATGACCTCAC	GGAAGATGGG	ACGAGGCCTC	AGGCATGAC	ATAGCCGCAG	CAGGCAGGAG	1080
CGCTCCTCTT	CAGCGTAGCT	CTCCACCTCT	ACCCGGAAACA	CACCCCTCTCA	CAGACGTACC	1140
AATGTTATT	TTATAATTTC	ATGGATTTAG	TTATACATAC	CTTAATAGTT	TTATAAAATT	1200
GTTGACATT	CAGGCAAATT	TGGCCAATAT	TATCATTGAA	TTTCTGTGT	TGGATTTCCT	1260
CTAGGATTTC	GCCAGTTCC	ACAAACGTGCA	GTAGGGCGGC	GGTAGCTCTT	GTGTCTGTGG	1320
ACTCTGCTCA	GCTGTGTC	TAGGAGTCGG	ATGTGTCTGT	GCTTATTAT	GGCCTTGT	1380
ATATATCACT	GAGGTATACT	ATGCCATGTA	AATAGACTAT	TTTTTATAAT	CTTAACATGC	1440

TGGTTAAAT	TCAGAAGGAA	ATAGATCAAG	GAAATATATA	TATTTCTTC	TAAAACCTAT	1500
TAAATTCTGT	TGACAAATAA	TCATTTCAT	CTTGGCAGCA	AAAAGTTCTC	AGTGACCTAT	1560
TTTGTGGTGT	TTCTTTTGA	AAAGAAAAGC	TGAAATATTA	TTAAATGCTA	GTATGTTCT	1620
GCCCATTATG	AAAGATGAAA	TAAAGTATTTC	AAAATATTAA	AAAAAAA	AAAAAATTCC	1680
TGCGGCCGC						1689

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCGGCA	CGAGGGAGCAG	ATCTGCAAGA	GTTCGTTTA	TGGAGGCTGC	TTGGGCAACA	60
AGAACAACTA	CCTTCGGGAA	GAAGAGTGCA	TTCTAGCCTG	TCGGGGTGTG	CAAGGTGGGC	120
CTTGTGAGAGG	CAGCTCTGGG	GCTCAGGCGA	CTTCCCCCA	GGGCCCCCTCC	ATGGAAAGGC	180
GCCATCCAGT	GTGCTCTGGC	ACCTGTCAGC	CCACCCAGTT	CCGCTGCAGC	AATGGCTGCT	240
GCATCGACAG	TTTCCTGGAG	TGTGACGACA	CCCCCAACTG	CCCCGACGCC	TCCGACGAGG	300
CTGCCTGTGA	AAAATACACG	AGTGGCTTG	ACGAGCTCCA	GCGCATCCAT	TTCCCCAGCG	360
ACAAAGGGCA	CTGCGTGAC	CTGCCAGACA	CAGGACTCTG	CAAGGAGAGC	ATCCCCCGCT	420
GGTACTACAA	CCCCTTCAGC	GAACACTGCG	CCCGCTTAC	CTATGGTGGT	TGTTACGGCA	480
ACAAGAACAA	CTTTGAGGAA	GAGCAGCAGT	GCCTCGAGTC	TTGTCGCGGC	ATCTCCAAGA	540
AGGATGTGTT	TGGCCTGAGG	CGGGAAATCC	CCATTCCCAG	CACAGGCTCT	GTGGAGATGG	600
CTGTCGCAGT	GTTCCTGGTC	ATCTGCATTG	TGGTGGTGGT	AGCCATCTTG	GGTTACTGCT	660
TCTTCAAGAA	CCAGAGAAAG	GACTTCCACG	GACACCACCA	CCACCCACCA	CCCACCCCTG	720
CCAGCTCCAC	TGTCTCCACT	ACCGAGGACA	CGGAGCACCT	GGTCTATAAC	CACACCACGC	780
GGCCCTCTG	AGCCTGGGTC	TCACCGGCTC	TCACCTGGCC	CTGCTTCCTG	CTTGCCAAGG	840
CAGAGGCCTG	GGCTGGGAAA	AACTTTGGAA	CCAGACTCTT	GCCTGTTTCC	CAGGCCCACT	900
GTGCCTCAGA	GACCAGGGCT	CCAGCCCCCTC	TTGGAGAAGT	CTCAGCTAAG	CTCACGTCT	960
GAGAAAGCTC	AAAGGTTTGG	AAGGAGCAGA	AAACCCCTGG	GCCAGAAGTA	CCAGACTAGA	1020
TGGACCTGCC	TGCATAGGAG	TTGGAGGAA	GTTGGAGTTT	TGTTTCCTCT	GTTCAAAGCT	1080
GCCTGTCCCT	ACCCCATGGT	GCTAGGAAGA	GGAGTGGGGT	GGTGTCAAGAC	CCTGGAGGCC	1140
CCAACCCCTGT	CCTCCCGAGC	TCCTCTTCCA	TGCTGTGCGC	CCAGGGCTGG	GAGGAAGGAC	1200
TTCCCTGTGT	AGTTTGTGCT	GTAAAGAGTT	GCTTTTGTT	TATTTAATGC	TGTGGCATGG	1260
GTGAAGAGGA	GGGGAAAGAGG	CCTGTTGGC	CTCTCTATCC	TCTCTTCCTC	TTCCCCCAAG	1320
ATTGAGCTCT	CTGCCCTTGA	TCAGCCCCAC	CCTGGCCTAG	ACCAGCAGAC	AGAGCCAGGA	1380
GAAGCTCAGC	TGCATTCCGC	AGCCCCCACC	CCCAAGGTTTC	TCCAACATCA	CAGCCCAGCC	1440
CGCCCACTGG	GTAATAAAAG	TGGTTGTGG	AAAAAAA	AAAAAAA	AAGTCCTGCG	1500
GCCGC						1505

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2002 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCGGCA	CGAGGGCCAT	GGCCGGGCTA	TCCCGCGGGT	CCGCGCGCGC	ACTGCTCGCC	60
GCCCTGCTGG	CGTCGACGCT	GTTGGCGCTG	CTCGTGTGCG	CCGCGCGGGG	TCGCGGCCGC	120

CGGGACCACG	GGGACTGGGA	CGAGGCCTCC	CGGCTGCCGC	CGCTACCACC	CCGCGAGGAC	180
CGGGCGCG	TGGCCCGCTT	CGTGACGCAC	GTCTCCGACT	GGGGCGCTCT	GGCCACCATC	240
TCCACGCTGG	AGGCGGTGC	CGGCCGGCCC	TCGCCTGACG	TCCTCTCGCT	CAGCGACGGG	300
CCCCCGGGCG	CGGGCAGCGG	CGTGCCTAT	TTCTACCTGA	GCCCGCTGCA	GCTCTCCGTG	360
AGCAACCTGC	AGGAGAATCC	ATATGCTACA	CTGACCATGA	CTTGGCACA	GACCAACTTC	420
TGCAAGAAC	ATGGATTG	TCCACAAAGT	CCCCTTGTG	TTCACATAAT	GCTGTCAGGA	480
ACTGTGACCA	AGGTGAATGA	AACAGAAATG	GATATTGCAA	AGCATTGTT	ATTCATTCGA	540
CACCCCTGAGA	TGAAAACCTG	GCCTTCCAGC	CATAATTGGT	TCTTGCTAA	GTTGAATATA	600
ACCAATATCT	GGGTCTGGA	CTACTTTGGT	GGACCAAAAA	TCGTGACACC	AGAAGAATAT	660
TATAATGTCA	CAGTTCACTG	AAGCAGACTG	TGGTGAATT	AGCAACACTT	ATGAAGTTTC	720
TTAAAGTGGC	TCATACACAC	TTAAAAGGCT	TAATGTTCT	CTGGAAAGCG	TCCCAGAATA	780
TTAGCCAGTT	TTCTGTACA	TGCTGGTTG	TTTGCTTGCT	TGTTTACTTG	CTTGTTCACC	840
AATAGAGTTG	ACCTGTTATT	GGATTTCCTG	GAAGATGTGG	TAGCTACTTT	TTTCCTATT	900
TGAAGCCATT	TTCTGTAGAGA	AATATCCTTC	ACTATAATCA	AATAAGTTT	GTCCCCATCAA	960
TTCCAAAGAT	GTTCAGTG	GTGCTCTG	AGAGGAATGA	GTACCAGTTT	TAAATTGCC	1020
ATTGGCATT	GAAGGTAGTT	GAGTATGTGT	TCTTATTCC	TAGAAGCCAC	TGTGCTTGGT	1080
AGAGTGCATC	ACTCACCACA	GCTGCCTCTT	GAGCTGCCTG	AGCCTGGTGC	AAAAGGATTG	1140
GCCCCCATTA	TGGTGCTCT	GAATAAATCT	TGCCAAGATA	GACAAACAAT	GATGAAACTC	1200
AGATGGAGCT	TCCTACTCAT	GTTGATTAT	GTCTCACAAT	CCTGGGTATT	GTTAATTCAA	1260
CATAGGGTGA	AACTATTCT	GATAAAGAAC	TTTGAAAAAA	CTTTTTATAC	TCTAAAGTGA	1320
TACTCAGAAC	AAAAGAAAGT	CATAAAACTC	CTGAATTAA	TTTCCCCACC	TAAGTCGAGA	1380
CAGTATTATC	AAAACACATG	TGCAACACAGA	TTATTTTTG	GCTCCAAAAC	TGGATTGCAA	1440
AAGAAAGAGG	AGAGATATT	TGTGTGTTCC	TGGTATTCTT	TTATAAGTAA	AGTTACCCAG	1500
GCATGGACCA	GCTTCAGCCA	GGGACAAAAT	CCCCTCCCAA	ACCACTCTCC	ACAGCTTTT	1560
AAAAATACTT	CTACTCTTAA	CAATTACCTA	AGGTTCCCTC	AAACCCCCCC	AACTCTTAAT	1620
AGCTCTAGT	GCTGCTACAA	TCTAAGTCAG	GTCACCAGAG	GGAAGAGAAC	ATGGCATTAA	1680
AAGAATCACA	TCTTCAGAAC	AGAAGACACT	AATATTATTA	CCCATATACA	TGATTCAGA	1740
AGATGACATA	AGATTCCCT	AAAGAGGAA	ATGTCAGGAA	TCAAGCCACT	GAATCCTTAA	1800
AGAGAAAAGT	TGAATATGAG	TCATTGTGTC	TGAAAACCTGC	AAAGTGAAC	TAACTGAGAT	1860
CCAGCAAACA	GGTTCTGTT	AAGAAAATA	ATTTATACTA	AATTTAGTAA	AATGGACTTC	1920
TTATTCAAAG	CATCAATAAT	AAAAAGAATT	ATTTTAAAAA	AAAAAAA	AAAAAAA	1980
AAAAAAAAT	TCCTGCAGGCC	GC				2002

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCCGGCA	CGAGGGCCAC	GACTCTGCTG	GCATTTCTTC	TATGCCACT	GGAATCTGAT	60
CCTGATTGTC	TTCCCACTACT	ACCAGGCCAT	CACCACTCCG	CCTGGGTACC	CACCCAGGG	120
CAGGAATGAT	ATCGCCACCG	TCTCCATCTG	TAAGAAGTGC	ATTTACCCCA	AGCCAGCCCG	180
AACACACCAC	TGCAGCATCT	GCAACAGGTG	TGTGCTGAAG	ATGGATCACC	ACTGCCCTG	240
GCTAAACAAT	TGTGTGGGCC	ACTATAACCA	TCGGTACTTC	TTCTCTTCT	GCTTTTCAT	300
GACTCTGGGC	TGTGTCTACT	GCAGCTATGG	AAGTTGGAC	CTTTTCCGGG	AGGCTTATGC	360
TGCCATTGAG	AAAATGAAAC	AGCTCGACAA	GAACAAACTA	CAGGCGGTTG	CCAACCAGAC	420
TTATCACCA	ACCCCACAC	CCACCTTCTC	CTTTCGAGAA	AGGATGACTC	ACAAGAGTCT	480
TGTCTACCTC	TGGTTCCCTG	GCAGTTCTGT	GGCACTTGCC	CTGGGTGCC	TAACTGTATG	540
GCATGCTGTT	CTCATCAGTC	GAGGTGAGAC	TAGCATCGAA	AGGCACATCA	ACAAGAAGGA	600
GAGACGTGCG	CTACAGGCCA	AGGGCAGAGT	ATTTAGGAAT	CCTTACAAC	ACGGCTGCTT	660
GGACAACCTGG	AAGGTATTCC	TGGGTGTGGA	TACAGGAAGG	CACTGGCTTA	CTCGGGTGCT	720
CTTACCTTCT	ACTCACTTGC	CCCATGGGAA	TGGAATGAGC	TGGGAGCCCC	CTCCCTGGGT	780

GACTGCTCAC	TCAGCCTCTG	TGATGGCAGT	GTGAGCTGGA	CTGTGTCAGC	CACGACTCGA	840
GCACTCATTC	TGCTCCCTAT	GTTATTTCAA	GGGCCTCCAA	GGGCAGCTTT	TCTCAGAATC	900
CTTGATCAAA	AAGAGCCAGT	GGGCCTGCCT	TAGGGTACCA	TGCAGGACAA	TTCAAGGACC	960
AGCCTTTTA	CCACTGCAGA	AGAAAGACAC	AATGTGGAGA	AATCTTAGGA	CTGACATCCC	1020
TTTACTCAGG	CAAACAGAAG	TTCCAACCCC	AGACTAGGGG	TCAGGCAGCT	AGCTACCTAC	1080
CTTGGCCAGT	GCTGACCCGG	ACCTCCTCCA	GGATACAGCA	CTGGAGTTGG	CCACCCACCTC	1140
TTCTACTTGC	TGTCTGAAAAA	AACACCTGAC	TAGTACAGCT	GAGATCTTGG	CTTCTCAACA	1200
GGGCAAAGAT	ACCAGGCCTG	CTGCTGAGGT	CACTGCCACT	TCTCACATGC	TGCTTAAGGG	1260
AGCACAAATA	AAGGTATTG	ATTTTAAAAA	AAAAAAAAAA	AAAAAAAAAT	TCCTGCGGCC	1320
GC						1322

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATTCGGCCA	CGAGGGAGCCT	GCCTTCATCT	AGGATGGCTC	CTCTGGGCAT	GCTGCTTGGG	60
CTGCTGATGG	CCGCCTGCTT	CACCTTCTGC	CTCAGTCATC	AGAACCTGAA	GGAGTTTGCC	120
CTGACCAACC	CAGAGAAGAG	CAGCACCAAA	GAAACAGAGA	GAAAAGAAC	CAAAGCCGAG	180
GAGGAGCTGG	ATGCCGAAGT	CCTGGAGGTG	TTCCACCCGA	CGCATGAGTG	GCAGGCCCTT	240
CAGCCAGGGC	AGGCTGTCCC	TGCAGGATCC	CACGTACGGC	TGAATCTTCA	GAATGGGAA	300
AGAGAGGCAA	AACTCCAATA	TGAGGACAAG	TTCCGAATA	ATTGAAAGG	CAAAAGGCTG	360
GATATCAACA	CCAACACCTA	CACATCTCG	GATCTCAAGA	GTGCACTGGC	AAAATTCAAG	420
GAGGGGGCAG	AGATGGAGAG	TTCAAAGGA	GACAAGGCAA	GGCAGGCTGA	GGTAAAGCGG	480
CTCTCCGCC	CCATTGAGGA	ACTGAAGAAA	GAATTGATG	AGCTGAATGT	TGTCAATTGAG	540
ACTGACATGC	AGATCATGGT	ACGGCTGATC	AACAAGTTCA	ATAGTTCCAG	CTCCAGTTG	600
GAAGAGAAGA	TTGCTGCGCT	CTTGATCTT	GAATATTATG	TCCATCAGAT	GGACAATGCG	660
CAGGACCTGC	TTTCCTTGG	TGGTCTTCAA	GTGGTGTATCA	ATGGGCTGAA	CAGCACAGAG	720
CCCCTCGTGA	AGGAGTATGC	TGCGTTTGTG	CTGGGCGCTG	CCTTTCCAG	CAACCCAAG	780
GTCCAGGTGG	AGGCCATCGA	AGGGGGAGCC	CTGCAGAACG	TGCTGGTCAT	CCTGGCCACG	840
GAGCAGCCGC	TCACTGCAA	GAAGAAGGTC	CTGTTGAC	TGTGCTCCCT	GCTGCCAC	900
TTCCCTATG	CCCAGCGGCA	GTTCTGAAG	CTCGGGGGC	TGCAAGTCCT	GAGGACCTG	960
GTGCAGGAGA	AGGGCACCGA	GGTGTGCGCC	GTGCGCGTGG	TCACACTGCT	CTACGACCTG	1020
GTCACGGAGA	AGATGTTGCG	CGAGGAGGAG	GCTGAGCTGA	CCCAGGAGAT	GTCCCCAGAG	1080
AAGCTGCAGC	AGTATCGCCA	GGTACACCTC	CTGCCAGGCC	TGTGGGAACA	GGGCTGGTGC	1140
GAGATCACGG	CCCACCTCCT	GGCGCTGCC	GAGCATGATG	CCCCTGAGAA	GGTGTGCGAG	1200
ACACTGGCG	TCCTCTGAC	CACCTGCC	GACCGCTACC	GTCAGGACCC	CCAGCTCGGC	1260
AGGACACTGG	CCAGCCTGCA	GGCTGAGTAC	CAGGTGCTGG	CCAGCCTGGA	GCTGCAGGAT	1320
GGTGAGGACG	AGGGCTACTT	CCAGGAGCTG	CTGGGCTCTG	TCAACAGCTT	GCTGAAGGAG	1380
CTGAGATGAG	GCCCCACACC	AGGACTGGAC	TGGGATGCCG	CTAGTGAGGC	TGAGGGGTGC	1440
CAGCGTGGGT	GGGCTTCTCA	GGCAGGAGGA	CATCTGGCA	GTGCTGGCTT	GGCATTAAA	1500
TGGAAACCTG	AAGGCCAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	1560
TTCCTGCGGC	CGC					1573

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTGGCA	CGAGGGGGCT	TTAAGGGACA	GCTGAGCCGG	CAGGTGGCAG	ATCAGATGTG	60
GCAGGCTGGG	AAAAGACAAG	CCTCCAGGGC	CTTCAGCTTG	TACGCCAAC	TCGACATCCT	120
CAGACCCTAC	TTTGATGTGG	AGCCTGCTCA	GGTGCAGAGC	AGGCTCCTGG	AGTCCATGAT	180
CCCTATCAAG	ATGGTCAACT	TCCCCCAGAA	AATTGCAGGT	GAACCTCTATG	GACCTCTCAT	240
GCTGGTCTTC	ACTCTGGTTG	CTATCCTACT	CCATGGGATG	AAGACGTCTG	ACACTATTAT	300
CCGGGAGGGC	ACCCCTGATGG	GCACAGCCAT	TGGCACCTGC	TTCCGGCTACT	GGCTGGGAGT	360
CTCATCCTTC	ATTTACTTCC	TTGCCTACCT	GTGCAACGCC	CAGATCACCA	TGCTGCAGAT	420
GTTGGCACTG	CTGGGCTATG	GCCTCTTGG	GCATTGCATT	GTCCCTGTTCA	TCACCTATAA	480
TATCCACCTC	CACGCCCTCT	TCTACCTCTT	CTGGCTGTTG	GTGGGTGGAC	TGTCCACACT	540
GCGCATGGTA	GCAGTGTGG	TGTCTCGGAC	CGTGGGCC	ACACAGCGGC	TGCTCCTCTG	600
TGGCACCCCTG	GCTGCCCTAC	ACATGCTCTT	CCTGCTCTAT	CTGCATTTG	CCTACCACAA	660
AGTGGTAGAG	GGGATCCTGG	ACACACTGGA	GGGCCCCAAC	ATCCCGCCCA	TCCAGAGGGT	720
CCCCAGAGAC	ATCCCTGCCA	TGCTCCCTGC	TGCTCGGCTT	CCCAACCACCG	TCCTCAACGC	780
CACAGCCAAA	GCTGTTGCGG	TGACCCCTGCA	GTCACACTGA	CCCCACCTGA	AATTCTTGGC	840
CAGTCCTCTT	TCCCGCAGCT	GCAGAGAGGA	GGAAGACTAT	TAAAGGACAG	TCCTGATGAC	900
ATGTTTCGTA	GATGGGGTTT	GCAGCTGCCA	CTGAGCTGTA	GCTGCGTAAG	TACCTCCTTG	960
ATGCCTGTCG	GCACTTCTGA	AAGGCACAAG	GCCAAGAACT	CCTGGCCAGG	ACTGCAAGGC	1020
TCTGCAGCCA	ATGCAGAAAA	TGGGTCAGCT	CCTTGAGAA	CCCCCTCCCCA	CCTACCCCTT	1080
CCTTCCTCTT	TATCTCTCCC	ACATTGTCTT	GCTAAATATA	GACTTGGTAA	TTAAAATGTT	1140
GATTGAAGTC	TGGAAAAAAA	AAAAAAAAAA	AATTCCCTGCG	GGCCGC		1185

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTGGCA	CGAGGCAAGC	CACCATCTTC	CTTCGGCCTG	CACCCCTTTA	AAGGCACCCA	60
GACCCCTCTG	GAAAAAGATG	AACTGAAGCC	CTTGACATC	CTCCAGCCTA	AGGAGTACTT	120
CCAGCTCAGC	CGCCACACGG	TCATTAAGAT	GGGAAGTGAG	AACGAGGCC	TGGATCTCTC	180
CATGAAGTCA	GTGCCCTGGC	TCAAGGCTGG	TGAAGTCAGT	CCCCAATCT	TCCAGGAAGA	240
TGCAGCCCTA	GACCTGTCAG	TGGCAGCCCA	CGGAAATCC	GAGCCTCCCC	CTGAGACACT	300
GTATGACAGT	GGTGCATCAG	TGGACAGCTC	AGGTACACACA	GTGATGGAGA	AACTTCCCAG	360
TGGCATGGAA	ATTCTTTTG	CCCCTGCCAC	GTCCCAGTAG	GCCCGAGCCA	TGATGGATAG	420
TCACATCAGC	AGCAGTGTAG	CTGCTACCGA	GATGCTCAGC	CAGCCCAACC	ACCCCAGCGG	480
CGAAGTCAAG	GCTGAAAATA	ACATTGAGAT	GGTGGGCGAG	TCCCAGGC	CCAAGGTCA	540
TGTCTCTGTC	GAAGATGCTG	TGCCTACCAT	ATTCTGTTG	AAGATCAAAG	GCCTCTCAGG	600
GGTGTCCACC	AAAAACTTCT	CCTTCAAAAG	AGAAGACTCC	GTGCTTCAGG	GCTATGACAT	660
CAACAGCCAA	GGGGAAGAGT	CCATGGGAAA	TGCAGAGCCC	CTTAGGAAAC	CCATCAAAAA	720
CCGGAGCATA	AAGTTAAAGA	AAAGTGAAC	CCAGGAAGTA	CACATGCTCC	CAATCAAAAA	780
ACAACGGCTG	GCCACCTTTT	TTCCAAGAAA	GTAAATAACG	GCTTTTAA	ATTGTATGA	840
TTATAATATG	GGGAAAGGTG	CATTGGTTT	ATAAAAAGGC	ATTAAAACA	AATTATCTT	900
GTAAATTATT	TTGGGGAGTA	GTTGGGAAAT	GGAAAGGTGA	ATTGGCTCTA	GAGGCCCTGT	960
ATGCTAGTAT	CATTTCTTT	TTAATT	GACTTTAC	AAATGAGTAA	ATAAGAGCAA	1020
CCTATTTTC	AAGCAGATG	CACATTTTT	GCAGCTTAA	TGGAATATTG	GGTGAATTAG	1080
AGGGGTAAAA	AAAGCTATT	TCATTGCCAC	AAAGTGCTT	GATGATGTAA	TACCTAATAA	1140
AGGGTAGGAT	GAATATTCA	CAATAATGT	TTGTTGCAC	AAAAAA	AAAAAA	1200
AAAAAA	AAATTCCCTGC	GGCCGC				1226

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAATTCTGGCA	CGAGGGCGCC	ATGGTGAAGG	TGACGTTCAA	CTCCGCTCTG	GCCCAGAAGG	60
AGGCCAAGAA	GGACGAGCCC	AAGAGCGGCG	AGGAGGCCT	CATCATCCCC	CCCGACGCCG	120
TCGCGGTGGA	CTGCAAGGAC	CCAGATGATG	TGGTACCAGT	TGGCCAAAGA	AGAGCCTGGT	180
GTTGGTGCAT	GTGCTTTGGA	CTAGCATTAA	TGCTTGCAGG	TGTTATTCTA	GGAGGAGCAT	240
ACTTGTACAA	ATATTTGCA	CTTCAACCAG	ATGACGTGTA	CTACTGTGGA	ATAAAAGTACA	300
TCAAAGATGA	TGTCATCTTA	AATGAGCCCT	CTGCAGATGC	CCCAGCTGCT	CTCTACCAGA	360
CAATTGAAGA	AAATATTAAA	ATCTTGAAG	AAGAAGAAGT	TGAATTATAC	AGTGTGCCTG	420
TCCCAGAGTT	TGCAGATAGT	GATCCTGCCA	ACATTGTTCA	TGACTTTAAC	AAGAAACTTA	480
CAGCCTATT	AGATCTTAAC	CTGGATAAGT	GCTATGTGAT	CCCTCTGAAC	ACTTCCATTG	540
TTATGCCACC	CAGAAACCTA	CTGGAGTTAC	TTATTAACAT	CAAGGCTGGA	ACCTATTGTC	600
CTCAGTCCTA	TCTGATTCTA	GAGCACATGG	TTATTACTGA	TCGCATTGAA	AACATTGATC	660
ACCTGGGTTT	CTTTATTAT	CGACTGTGTC	ATGACAAGGA	AACTTACAAA	CTGCAACGCA	720
GAGAAACTAT	TAAAGGTATT	CAGAAACGTG	AAGCCAGCAA	TTGTTTCGCA	ATTCGGCATT	780
TTGAAAACAA	ATTTGCCGTG	GAAACTTAA	TTTGTTCCTG	AACAGTCAAG	AAAAACATTA	840
TTGAGGAAAA	TTAATATCAC	AGCATAACCC	CACCCATTAC	ATTTGTTGC	AGTTGATTAT	900
TTTTAAAGT	CTTCTTTCAT	GTAAGTAGCA	AACAGGGCTT	TACTATCTTT	TCATCTCATT	960
AATTCAATTAA	AAACCATTAC	CTTAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	1020
AAAAAAAAAA	AAAAAATTCC	TGCGGCCGC				1049

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAATTCTGGCA	CGAGGGGAGA	ATACTTTTG	CGATGCCTAC	TGGAGACTTT	GATTGAAAGC	60
CCAGTTGGGC	CGACCAGGTG	GAGGAGGAGG	GGGAGGACGA	CAAATGTGTC	ACCAGCGAGC	120
TCCTCAAGGG	GATCCCTCTG	GCCACAGGTG	ACACCAGCCC	AGAGCCAGAG	CTACTGCCGG	180
GAGCTCCACT	GCCGCCTCCC	AAGGAGGTCA	TCAACGGAAA	CATAAAGACA	GTGACAGAGT	240
ACAAGATAGA	TGAGGATGGC	AAGAAGTTCA	AGATTGTCG	CACCTTCAGG	ATTGAGACCC	300
GGAAGGCTTC	AAAGGCTGTC	GCAAGGAGGA	AGAACTGGAA	GAAGTTCGGG	AACTCAGAGT	360
TTGACCCCCC	CGGACCCAAT	GTGCCACCA	CCACTGTCA	TGACGATGTC	TCTATGACGT	420
TCATCACCAAG	CAAAGAGGAC	CTGAAC TGCC	AGGAGGAGGA	GGACCCCTATG	AAACAAATTCA	480
AGGGCCAGAA	GATCGTGTC	TGCCGCATCT	GCAAGGGCGA	CCACTGGACC	ACCCGCTGCC	540
CCTACAAGGA	TACGCTGGGG	CCCATGCAGA	AGGAGCTGGC	CGAGCAGCTG	GGCCTGTCTA	600
CTGGCGAGAA	GGAGAAGCTG	CCGGGAGAGC	TAGAGCCGGT	GCAGGCCACG	CAGAACAAAGA	660
CAGGGAAGTA	TGTGCCGCCG	AGCCTGCGCG	ACGGGGCCAG	CCGCCGCCGGG	GAGTCCATGC	720
AGCCCAACCG	CAGAGCCGAC	GACAACGCCA	CCATCCGTGT	CACCAACTTG	CGCAGAGGAC	780
ACGCGTGAGA	CCGACCTGCA	GGAGCTCTTC	CGGCCTTTCG	GCTCCATCTC	CCGCATCTAC	840
CTGGCTAAGG	ACAAGACCCAC	TGGCCAATCC	AAGGGCTTTG	CCTTCATCAG	CTTCCACCGC	900

CGCGAGGATG	CTGCGCGTGC	CATTGCCGGG	GTGTCCGGCT	TTGGCTACGA	CCACCTCATC	960
CTCAACGTCG	AGTGGGCCAA	GCCGTCCACC	AACTAAGCCA	GCTGCCACTG	TGTACTCGGT	1020
CCGGGACCT	TGGCAGACAGA	AGACAGCCTC	CGAGAGCGCG	GGCTCCAAGG	GCAATAAAGC	1080
AGCTCCACTC	TCAAAAAAAA	AAAAAAA	AAAAAAA	AAAAAAAAT	TCCTGCGGCC	1140
GC						1142

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAATTCCGGCA	CGAGGGAAAC	ATGGCGGTAG	GCTGGGACCA	TAACACAAGC	ATGACTATAT	60
GAAGGAAGAG	GAAGGTTTTC	CTGAAGATGA	GGCGACTGAA	TCGGAAAAAA	ACTTTAAGTT	120
TGGTAAAAGA	GTTGGATGCC	TTTCCGAAGG	TTCCCTGAGAG	CTATGTAGAG	ACTTCAGCCA	180
GTGGAGGTAC	AGTTTCTCTA	ATAGCATTAA	CAACTATGGC	TTTATTAACC	ATAATGGAAT	240
TCTCAGTATA	TCAAGATACA	TGGATGAAGT	ATGAATACGA	AGTAGACAAG	GATTTTCTA	300
GCAAATTAAG	AATTAATATA	GATATTACTG	TTGCCATGAA	GTGTCATAT	GTTGGAGCGG	360
ATGTATTGGA	TTTAGCAGAA	ACAATGGTTG	CATCTGCAGA	TGGTTTAGTT	TATGAACCAA	420
CAGTATTGTA	TCTTCACCA	CAGCAGAAAG	AGTGGCAGAG	GATGCTGCAG	CTGATTTCAGA	480
GTAGGCTACA	AGAAGAGCAT	TCACTTCAAG	ATGTGATATT	TAAAAGTGCT	TTTAAAAGTA	540
CATCAACAGC	TCTTCCACCA	AGAGAAGATG	ATTCATCACA	GTCTCCAAAT	GCATGCAGAA	600
TTCATGGCCA	TCTATATGTC	AATAAAGTAG	CAGGGAATT	TCACATAACA	GTGGGCAAGG	660
CAATTCACCA	TCCTCGTGGT	CATGCACATT	TGGCAGCACT	TGTCAACCAT	GAATCTTACA	720
ATTTTTCTCA	TAGAATAGAT	CATTGTCTT	TTGGAGAGCT	TGTTCCAGCA	ATTATTAATC	780
CTTTAGATGG	AACTGAAAAA	ATTGCTATAG	ATCACAACCA	GATGTTCCAA	TATTTTATTA	840
CAGTTGTGCC	AAACAAACTA	CATACATATA	AAATATCAGC	AGACACCCAT	CAGTTTCTG	900
TGACAGAAAG	GGAACGTATC	ATTAACCATG	CTGCAGGCAG	CCATGGAGTC	TCTGGGATAT	960
TTATGAAATA	TGATCTCAGT	TCTCTTATGG	TGACAGTTAC	TGAGGAGCAC	ATGCCATTCT	1020
GGCAGTTTT	TGTAAGACTC	TGTGGTATTG	TTGGAGGAAT	CTTTTCAACA	ACAGGCATGT	1080
TACATGGAAT	TGGAAAATT	ATAGTTGAAA	TAATTTGCTG	TCGTTTCAGA	CTTGGATCCT	1140
ATAAACCTGT	CAATTCTGTT	CCTTTGAGG	ATGCCACAC	AGACAACCCAC	TTACCTCTTT	1200
TAGAAAATAA	TACACATAA	CACCTCCCGA	TTGAAGGAGA	AAAACTTTT	GCCTGAGACA	1260
TAAAACCTTT	TTTTAATAAT	AAAATATTGT	GCAATATATT	CAAAGAAAAG	AAAACACAAA	1320
TAAGCAGAAA	ACATACTTAT	TTTAAAAAAAG	AAAAAAAAGG	ATAAAAAAAC	CCAAACTGAA	1380
ATTCTATATA	CGTTGTGTCT	GTTACAAATG	TCGTAGAAGA	AATCATGCAG	CTAAACGATG	1440
AAGAAGCCCA	ACTGGAGTGT	TGCTTTGAAG	ATGACGCCCT	CTTATATTCTT	CATAGCAAAT	1500
GGGTGGTATC	AAAATCAGAC	ATTGCTTCTT	GCTGATAAAA	AGCCTGAAGG	AAATAAGTGA	1560
AACTACATCT	ATGGGAAAAA	AAAAAACATT	GAGAAGTGCA	AATGTTCGCA	TCCTTTGTT	1620
TTTAAAAGAT	ATGATGTCAG	AATAAAATGT	GGAAAACATA	CGGAAAAAAA	AAAAAAA	1680
AAATTCCCTGC	GGCCGC					1696

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAATTCTGGCA	CGAGGGCGGCA	CGAGGGCGGCA	CGAGGGTGGC	ATATCACGGC	CATGGGTCT	60
CAGCATTCCG	CTGCTGCTCG	CCCTCCTCC	TGCAGGGAA	AGCAAGAAGA	TGACAGGGAC	120
GGTTGCTGG	CTGAACGAGA	GCAGGAAGAA	GCCATTGCTC	AGTCCCATA	TGTGGAATT	180
ACCAGGGAGAG	ATAGCATCAC	CTGCTCACG	TGCCAGGGGA	CAGGCTACAT	TCCAACAGAG	240
CAAGTAAATG	AGTTGGTGGC	TTTGATCCCA	CACAGTGATC	AGAGATTGCG	CCCTCAGCGA	300
ACTAAGCAAT	ATGTCTCTCT	GTCCATCCTG	CTTTGTCCTC	TGGCATCTGG	TTTGGTGGTT	360
TTCTCCCTGT	TTCCGATTC	AGTCCTTGTG	GATGATGACG	GCATCAAAGT	GGTGAAAGTC	420
ACATTTAATA	AGCAAGACTC	CCTTGTATT	CTCACCATCA	TGGCCACCCCT	AAAAATCAGG	480
AACTCCAATC	TCTACACGGT	GGCAGTGACC	AGCCTGTCCA	GCCAGATTCA	GTACATGAAC	540
ACAGTGGTCA	GTACATATGT	GACTACTAAC	GTCTCCCTTA	TTCCACCTCG	GAGTGAGCAA	600
CTGGTGAATT	TTACCGGGAA	GGCCGAGATG	GGAGGACCGT	TTTCCTATGT	GTACTTCTTC	660
TGCACGGTAC	CTGAGATCCT	GGTGCACAAAC	ATAGTGATCT	TCATGCGAAC	TTCAGTGAAG	720
ATTTCATACA	TTGGCCTCAT	GACCCAGAGC	TCCTTGGAGA	CACATCACTA	TGTGGATTGT	780
GGAGGAAATT	CCACAGCTAT	TTAACAAACTG	CTATTGGTTC	TTCCACACAG	CGCCTGTAGA	840
AGAGAGCACA	GCATATGTTC	CCAAGGCCTG	AGTTCTGGAC	CTACCCCCAC	GTGGTGTAAAG	900
CAGAGGAGGA	ATTGGTTCAC	TTAACCTCCA	GCAAACATCC	TCCTGCCACT	TAGGAGGAAA	960
CACCTCCCTA	TGGTACCAATT	TATGTTCTC	AGAACCGAGCA	GAATCAGTGC	CTAGCCTGTG	1020
CCCAGCAAAT	AGTTGGCACT	CAATAAAGAT	TTGCAGAATT	AAAAAAAAAA	AAAAAAAAAA	1080
AAAAAAATTC	CTGCGGCCGC					1100

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAATTCTGGCA	CGAGGGTACC	TGCTTTCTA	TTGCCTCTTT	GAAACAATGG	TCACGTGTTT	60
CCATGTTCCC	TACTCGGCTC	TCACCATGTT	CATCAGCACC	GAGCAGACTG	AGCAGGGATTC	120
TGCCACCGCC	TATCGGATGA	CTGTGGAAGT	GCTGGGCACA	GTGCTGGGCA	CGGCGATCCA	180
GGGACAAATC	GTGGGCCAAG	CAGACACGCC	TTGTTCCAG	GACCTCAATA	GCTCTACAGT	240
AGCTTCACAA	AGTGCCAAC	ATACACATGG	CACCACTCA	CACAGGGAAA	CGAAAAGGC	300
ATACCTGCTG	GCAGCGGGGG	TCATTGCTG	TATCTATATA	ATCTGTGCTG	TCATCCTGAT	360
CCTGGGCGTG	CGGGAGCAGA	GAGAACCTTA	TGAAGCCCAG	CAGTCTGAGC	CAATCGCCTA	420
CTTCCGGGGC	CTACGGCTGG	TCATGAGCCA	CGGCCCATAC	ATCAAACTTA	TTACTGGCTT	480
CCTCTTCACC	TCCTTGGCTT	TCATGCTGGT	GGAGGGGAAC	TTTGTCTTGT	TTTGCACCTA	540
CACCTTGGGC	TTCCGCAATG	AATTCCAGAA	TCTACTCCTG	GCCATCATGC	TCTCGGCCAC	600
TTTAACCATT	CCCATCTGGC	AGTGGTCTT	GACCCGGTTT	GGCAAGAAGA	CAGCTGTATA	660
TGTTGGGATC	TCATCAGCAG	TGCCATTCT	CATCTGGTG	GCCCTCATGG	AGAGTAACCT	720
CATCATTACA	TATGCGGTAG	CTGTGGCAGC	TGGCATCAGT	GTGGCAGCTG	CCTTCTTA	780
ACCCGGTCC	ATGCTGCCTG	ATGTCATTGA	CGACTTCCAT	CTGAAGCAGC	CCCACTTCCA	840
TGGAACCGAG	CCCATCTCT	TCTCCTTCTA	TGTCTTCTTC	ACCAAGTTG	CCTCTGGAGT	900
GTCACTGGGC	ATTTCACCC	TCAGTCTGGA	CTTTCAGGG	TACCAGACCC	GTGGCTGCTC	960
GCAGCCGGAA	CGTGTCAAGT	TTACACTGAA	CATGCTCGTG	ACCATGGCTC	CCATAGTTCT	1020
CATCCTGCTG	GGCCTGCTGC	TCTCAAAAT	GTACCCATT	GATGAGGAGA	GGCGGCGGCA	1080
GAATAAGAAG	GCCCTGCAGG	CACTGAGGGA	CGAGGCCAGC	AGCTCTGGCT	GCTCAGAAC	1140
AGACTCCACA	GAGCTGGCTA	GCATCCTCTA	GGGCCCGCCA	CGTTGCCCGA	AGCCACCATG	1200
CAGAAGGCCA	CAGAAGGGAT	CAGGACCTGT	CTGCCGGCTT	GCTGAGCAGC	TGGACTGCAG	1260
GTGCTAGGAA	GGGAACGTGAA	GACTCAAGGA	GGTGGCCAG	GACACTTGCT	GTGCTCACTG	1320
TGGGGCCGGC	TGCTCTGTGG	CCTCCTGCCT	CCCCTCTGCC	TGCCGTGAGG	GCCAAGCCCT	1380
GGGGCTGCCA	CTGTGAATAT	GCCAAGGACT	GATCGGGCCT	AGCCCGGAAC	ACTAATGTAG	1440
AAACCTTTT	TTTACAGAGC	CTAATTAATA	ACTTAATGAC	TGTGTACATA	GCAATGTGTG	1500

TGTATGTATA TGTCTGTGAG CTATTAATGT TATTAATTCTT CATAAAAGCT GGAAAGCAAA	1560
AAAAAAAAAAA AAAAATTCTT CGGGCCGC	1588

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCGGCA CGAGGCGGAA GTCCCGTCTC ACGGTTGCCCG TGGCAGCGCG CGAGGCTGGT	60
GAGTCGGCAG CCCTGTGGCA GCCGGCGGGC TGGTTTCCAT GGTTGCACGA TTAGGAACCA	120
CCAGCTGCTG CATCCCCTGG CCAGGGGTGG CGTCCAGGTG GCAGAGCAGC TAGGAACGCA	180
AGGCCTGAAC CTGGGGCCAG ACACCCTGCT CTCCCGGCCA TGGTCAACGA CCCTCCAGTA	240
CCTGCCCTAC TGTGGGCCCA GGAGGTGGGC CAAGTCTTGG CAGGCCGTGC CCGCAGGCTG	300
CTGCTGCAGT TTGGGGTGCT CTTCTGCACC ATCCTCCTT TGCTCTGGGT GTCTGTCTTC	360
CTCTATGGCT CCTTCTACTA TTCTATATG CCGACAGTCA GCCACCTCAG CCCTGTGCAT	420
TTCTACTACA GGACCGACTG TGATTCTCC ACCACCTCAC TCTGCTCCTT CCCTGTTGCC	480
AATGTCTCGC TGACTAAGGG TGGACGTGAT CGGGTGCCTGA TGTATGGACA GCCGTATCGT	540
GTTACCTTAG AGCTTGAGCT GCCAGAGTCC CCTGTAATC AAGATTTGGG CATGTTCTG	600
GTCACCATTG CCTGCTACAC CAGAGGTGGC CGAACATCT CCACCTCTTC GCGTTGGTG	660
ATGCTGCATT ACCGCTCAGA CCTGCTCCAG ATGCTGGACA CACTGGTCTT CTCTAGCCTC	720
CTGCTATTG GCTTGCAGA GCAGAAGCAG CTGCTGGAGG TGGAACTCTA CGCAGACTAT	780
AGAGAGAACT CGTACGTGCC GACCACTGGA GCGATCATT AGATCCACAG CAAGCGCATC	840
CAGCTGTATG GAGCCTACCT CCGCATCCAC GCGCACTTCA CTGGGCTCAG ATACCTGCTA	900
TACAACATTCC CGATGACCTG CGCCTTCATA GGTGTTGCCA GCAACTTCAC CTTCCTCAGC	960
GTCATCGTGC TCTTCAGCTA CATGCACTGG GTGTGGGGGG GCATCTGGCC CCGACACCGC	1020
TTCTCTTGC AGGTTAACAT CGAAAAAAGA GACAATTCCC GGAAGGAAGT CCAACGAAGG	1080
ATCTCTGCTC ATCAGCCAGG GCCTGAAGGC CAGGAGGAGT CAACTCCGCA ATCAGATGTT	1140
ACAGAGGATG GTGAGAGCCC TGAAGATCCC TCAGGGACAG AGGTCAGCTG TCCGAGGAGG	1200
AGAAAACCAGA TCAGCAGCCC CTGAGCGGAG AAGAGGAGCT AGAGCCTGAG GCCAGTGATG	1260
GTTCAGGCTC CTGGGAAGAT GCAGCTTGC TGACGGAGGC CAAACCTGCCT GCTCCTGCTC	1320
CTGCTTCTGC TTCTGCCCT GTCTAGAGA CTCTGGCAG CTCTGAACCT GCTGGGGTG	1380
CTCTCCGACA GCGCCCCACC TGCTCTAGTT CCTGAAGAAA AGGGGCAGAC TCCTCACATT	1440
CCAGCACTT CCCACCTGAC TCCCTCTCCCC TCGTTTTCC TTCAATAAAC TATTTGTGT	1500
CAAAAAAAAAA AAAAAAAAAA AATTCCTGCG GCCGC	1535

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCGGCA CGAGGGCGGG CGCTACGGGC TTGACTCCCC CAAGGCCGAG GTCCGCGGCC	60
AGGTGCTGGC GCCGCTGCCCT CTCCACGGAG TTGCTGATCA TCTGGGCTGT GATCCACAAA	120
CCCGGTTCTT TGTCCCTCCT AATATCAAAC AGTGGATTGC CTTGCTGCAG AGGGGAAACT	180
GCACGTTAA AGAGAAAATA TCACGGGCCG CTTTCCACAA TGCAAGTTGCT GTAGTCATCT	240
ACAATAATAA ATCCAAAGAG GAGCCAGTTA CCATGACTCA TCCAGGCACT GGAGATATTA	300

TTGCTGTCAT	GATAACAGAA	TTGAGGGGTA	AGGATATTTT	GAGTTATCTG	GAGAAAAACA	360
TCTCTGTACA	AATGACAATA	GCTGTTGGAA	CTCGAATGCC	ACCGAAGAAC	TTCAGCCGTG	420
GCTCTCTAGT	CTTCGTGTCA	ATATCCTTA	TTGTTTGAT	GATTATTTCT	TCAGCATGGC	480
TCATATTCTA	CTTCATTCAA	AAGATCAGGT	ACACAAATGC	ACGCGACAGG	AACCAGCGTC	540
GTCTCGGAGA	TGCAGCCAAG	AAAGCCATCA	GTAAATTGAC	AACCAGGACA	GTAAAGAAGG	600
GTGACAAGGA	AACTGACCCA	GACTTGATC	ATTGTGCACT	CTGCATAGAG	AGCTATAAGC	660
AGAATGATGT	CGTCCGAATT	CTCCCTGCA	AGCATGTTT	CCACAAATCC	TGCGTGGATC	720
CCTGGCTTAG	TGAACATTGT	ACCTGTCTA	TGTGCAAAC	TAATATATTG	AAGGCCCTGG	780
GAATTGTGCC	GAATTGCCA	TGTACTGATA	ACGTAGCATT	CGATATGGAA	AGGCTCACCA	840
GAACCCAAGC	TGTTAACCGA	AGATCAGCCC	TCGGCGACCT	CGCCGGCGAC	AACTCCCTTG	900
GCCTTGAGCC	ACTTCGAACT	TCGGGGATCT	CACCTCTTCC	TCAGGATGGG	GAGCTCACTC	960
CGAGAACAGG	AGAAATCAAC	ATTGCACTAA	CAAAAGAATG	GTTTATTATT	GCCAGTTTG	1020
GCCTCCTCAG	TGCCCTCACA	CTCTGCTACA	TGATCATCAG	AGCCACAGCT	AGCTTGAATG	1080
CTAATGAGGT	AGAATGGTT	TGAAGAAGAA	AAAACCTGCT	TTCTGACTGA	TTTGCCCTTG	1140
AAGGAAAAAA	GAACCTATTT	TTGTGCATCA	TTTACCAATC	ATGCCACACA	AGCATTATT	1200
TTTAGTACAT	TTTATTTTTT	CATAAAATTG	CTAATGCCA	AGCTTTGTAT	AAAAGAAAT	1260
AAATAATAAA	ATAAAAAAA	AAAAAAA	AAAAAAA	AAAAAAAAT	TCCTGCGGCC	1320
GC						1322

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCGGC	CGAGGCCCTC	CCCGCGCTCCC	GGGGCGCGCG	GGCCGCGCCC	CCGACGCCCT	60
ACATATACTC	AGGTGCGCCC	CACCTGTCCG	CCCGCACCTG	CTGGCTCAC	TCCGAGCCAC	120
CTCTGCTCG	CACCGCAGCC	TCGGACCTAC	AGCCCAGGAT	ACTTTGGGAC	TTGCCGGCGC	180
TCAGAAACGC	GCCCAGACGG	CCCTCTCACC	TTTTGTTGC	CTAGGGTCGC	CGAGAGCGCC	240
CGGAGGGAAC	CGCCTGGCCT	TCGGGGACCA	CCAATTGTTG	CTGGAACACCAC	CCTCCGGCG	300
TATCCTACTC	CCTGTGCCGC	GAGGCCATCG	CTTCACTGGA	GGGGTCGATT	TGTGTGTAGT	360
TTGGTGACAA	GATTTGCATT	CACCTGGCCC	AAACCCCTTT	TGTCTCTTTG	GGTGACCGGA	420
AAACTCCACC	TCAAGTTTC	TTTGTGGGG	CTGCCCCCA	AGTGTGTTT	GTTTACTGT	480
AGGGTCTCCC	GCCCGGGGCC	CCCAGTGT	TCTGAGGGCG	GAATGGCCA	ATTGGGCC	540
GCAGTTGCTG	GGCTTCTCCA	TGGCCCTGCT	GGGCTGGGTG	GGTCTGGTGG	CCTGCACCGC	600
CATCCCGCAG	TGGCAGATGA	GCTCCTATGC	GGGTGACAAC	ATCATCACGG	CCCAGGCCAT	660
GTACAAGGGG	CTGTGGATGG	ACTGCGTCAC	GCAGAGCACG	GGGATGATGA	GCTGAAAAT	720
GTACGACTCG	GTGCTGCC	TGTCCGCGG	CTTGCAGGCC	ACTCGAGCCC	TAATGGTGGT	780
CTCCCTGGTG	CTGGGCTTCC	TGGGCATGTT	TGTGGCCACG	ATGGGCATGA	AGTGCACCG	840
CTGTGGGGGA	GACGACAAAG	TGAAGAAGGC	CCGTATAGCC	ATGGGTGGAG	GCATAATT	900
CATCGTGGCA	GGTCTTGC	CCTTGGTAGC	TTGCTCCTGG	TATGGCCATC	AGATTGTCAC	960
AGACTTTAT	AACCCTTGA	TCCCTACCAA	CATTAAGTAT	GAGTTGGCC	CTGCCATCTT	1020
TATTGGCTGG	GCAGGGTCTG	CCCTAGTCAT	CCTGGGAGGT	GCACTGCTCT	CCTGTTCTG	1080
TCCTGGGAAT	GAGAGCAAGG	CTGGGTACCG	TGCACCCCGC	TCTTACCCCTA	AGTCCAAC	1140
TTCCAAGGG	TATGTGTGAC	CTGGGATCTC	CTTGGCCCAG	CCTGACAGGC	TATGGGAGTG	1200
TCTAGATGCC	TGAAAGGGCC	TGGGGCTGAG	CTCAGCCTGT	GGGCAGGGTG	CCGGACAAAG	1260
GCCTCCTGGT	CACTCTGTCC	CTGCACTCCA	TGTATAGTCC	TCTTGGGTG	GGGGTGGGG	1320
GGTGCCGTG	GTGGGAGAGA	CAAAAAGAGG	GAGAGTGTG	TTTTGTACA	GTAAAGAAAA	1380
ATAAGTATTG	GGAAGCAGGC	TTTTTCCCT	TCAGGGCCTC	TGCTTCC	CCGTCCAGAT	1440
CCTTGCAGGG	AGCTTGGAAC	CTTAGTGCAC	CTACTTCAGT	TCAGAACACT	TAGCACCCCA	1500
CTGACTCCAC	TGACAATGA	CTAAAAGATG	CAGGTGCTCG	TATCTCGACA	TTCATTCCCA	1560
CCCCCTCTT	ATTTAAATAG	CTACCAAAGT	ACTTCTTTT	TAATAAAA	ATAAGATTT	1620

TTATTAGGTA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1680
AAAAAAAAAA AAAAAAAATT CCTGCGGCG C	1711

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTGGCA CGAGGGCAGG TCCAGAGTAA AGTCAGTCAA GAGTGGAAAGC GAGGAAGGAA	60
CAGGATGATT AGACCTCAGC TGCGGACCGC GGGGCTGGGA CGATGCCTCC TGCCGGGCT	120
GCTGCTGTC CTGGTGCCTCG TCCTCTGGGC CGGGGCTGAA AAGCTACATA CCCAGCCCTC	180
CTGCCCCGCG GTCTGCCAGC CCACCGCGCTG CCCACCTGCG CGCTGGGAC	240
CACGCCGGTG TTCGACCTGT GCCGCTGTTG CGCGCTCTGC CCCCGCGGCCG AGCGTGAAGT	300
CTGCGGCGGG GCGCAGGGCC AACCGTGCAGC CCCGGGGCTG CAGTGCCTCC AGCCGCTGCG	360
CCCCGGGTTG CCCAGCACCT GCGGTTGCC GACGCTGGGA GGGGCGGTGT GCGGCAGCGA	420
CAGGCGCACC TACCCCAGCA TGTGCGCGCT CGGGGCGAA AACCGCGCCG CGCGCCGCCT	480
GGGCAAGGTC CGGGCCGTGC CTGTGAGTG GGGGAACCTGC GGGGATAACAG GGACCAGAAG	540
CGCAGGCCCG CTCAGGAGGA ATTACAACCT CATGCCCGCG GTGGTGGAGA AGGTGGCGCC	600
ATCGGTGGTT CACGTGCAGC TGTGGGGCAG GTTACTTCAC GGCAGCAGGC TTGTTCTGT	660
GTACAGTGGC TCTGGGTTCA TAGTGTCTGA GGACGGGCTC ATTATTACCA ATGCCCATGT	720
TGTCAAGAAC CAGCAGTGGA TTGAGGTGGT GCTCCAGAAAT GGGGCCCCGTT ATGAAGCTGT	780
TGTCAAGGAT ATTGACCTTA ATTGGATCT TGCGGTGATT AAGATTGAAT CAAATGCTGA	840
ACTTCCTGTA CTGATGCTGG GAAGATCATC TGACCTTCGG GCTGGAGAGT TTGTGGTGGC	900
TTTGGGCAGC CCATTTCTC TGCAAGAACAC AGCTACTGCA GGAATTGTCA GCACCAAACA	960
GCGAGGGGGC AAAGAACCTGG GGATGAAGGA TTCAGATATG GACTACGTCC AGATTGATGC	1020
CACAATTAAC TATGGGAATT CTGGTGGTCC TCTGGTGAAC TTGGATGGTG ATGTGATTGG	1080
CGTCAATTCA TTGAGGGTGA CTGATGGAAT CTCCTTGCA ATTCTTCAG ATCGAGTTAG	1140
GCAGTTCTTG GCAGAATACC ATGAGCACCA GATGAAAGGA AAGGCCTTT CAAATAAGAA	1200
ATATCTGGGT CTGCAAATGC TGTCCCTCAC TGTCCCCCTT AGTGAAGAAT TGAAAATGCA	1260
TTATCCAGAT TCCCTGATG TGAGTTCTGG GTTTTATGTA TGAAAGTGG TTGAAGGAAC	1320
AGCTGCTCAA AGCTCTGGAT TGAGAGATCA CGATGTAATT GTCAACATAA ATGGGAAACC	1380
TATTACTACT ACAACTGATG TTGTTAAAGC TCTTGACAGT GATTCCCTTT CCATGGCTGT	1440
TCTTCGGGGA AAAGATAATT TGCTCCTGAC AGTCATACCT GAAACAATCA ATTAAATATC	1500
TTGTTTAAAGTGGATTAT CTAAAAAAAGA AAAAAAAAGA TTCTGCGGGC CGC	1553

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1596 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTGGCA CGAGGGGAGC CGCTCCCGGA GCCCCGGCGT AGAGGCTGCA ATCGCAGCCG	60
GGAGCCCGCA GCCCCGCGCC CGAGCCCGCC GCGGCCCTTC GAGGGCGCCC CAGGCCGCGC	120
CATGGTGAAG GTGACGTCA ACTCCGCTCT GGGCCAGAAAG GAGGCCAAGA AGGACGAGCC	180
CGAGAGCGGC GAGGAGGCAGC TCATCATCCC CCCCCGACGCC GTCGCGGTGG ACTGCAAGGA	240

CCCAGATGAT	GTGGTACCAAG	TTGGCCAAAG	AAGAGCCTGG	TGTGGTGCA	TGTGCTTGG	300
ACTAGCATT	ATGCTTGCAG	GTGTTATTCT	AGGAGGAGCA	TACCTGTACA	AATATTTGC	360
ACCTCAACCA	GATGACGTGT	ACTACTGTGG	AATAAAGTAC	ATCAAAGATG	ATGTCATCTT	420
AAATGAGCCC	TCTGCAGATG	CCCCAGCTGC	TCTCTACCAAG	ACAATTGAAG	AAAATATTAA	480
AATCTTGAA	GAAGAAGAAG	TTGAATTAT	CAGTGTGCCT	GTCCCAGAGT	TTGCAGATAG	540
TGATCCTGCC	AACATTGTT	ATGACTTTAA	CAAGAAACTT	ACAGCCTATT	TAGATCTTAA	600
CCTGGATAAG	TGCTATGTGA	TCCCTCTGAA	CACTTCCATT	GTTATGCCAC	CCAGAAACCT	660
ACTGGAGTTA	CTTATTAACA	TCAAGGCTGG	AACCTATTG	CCTCAGTCCT	ATCTGATTCA	720
TGAGCACATG	GTTATTACTG	ATCGCATTGA	AAACATTGAT	CACCTGGGTT	TCTTATTAA	780
TCGACTGTGT	CATGACAAGG	AAACTTACAA	ACTGCAACGC	AGAGAAACTA	TTAAAGGTAT	840
TCAGAAACGT	GAAGCCAGCA	ATTGTTTCGC	AATTGGGCAT	TTTAAAACA	AATTTGCCGT	900
GGAAACTTTA	ATTGTTCTT	GAACAGTCAA	GAAAACATT	ATTGAGGAAA	ATTAATATCA	960
CAGCATAACC	CCACCCCTTA	CATTGTTGTGC	AGTGATATT	TTTAAAGTCT	CTTTCATGTA	1020
AGTAGCAAAC	AGGGCTTAC	TATCTTTCA	TCTCATTAA	TCAATTAAAA	CCATTACCTT	1080
AAAATTTTT	TCTTCGAAG	TGTGGTGTCT	TTTATATTG	AATTAGTAAC	TGTATGAAGT	1140
CATAGATAAT	AGTACATGTC	ACCTTAGGTA	GTAGGAAGAA	TTACAATTTC	TTTAAATCAT	1200
TTATCTGGAT	TTTTATGTT	TATTAGCATT	TTCAAGAAGA	CGGATTATCT	AGAGAATAAT	1260
CATATATATG	CATACGTAA	AATGGACCAC	AGTGACTTAT	TTGTAGTTGT	TAGTTGCCCT	1320
GCTACCTAGT	TTGTTAGTGC	ATTGAGCAC	ACATTTAA	TTCCCTCTAA	TTAAAATGTG	1380
CAGTATTTTC	AGTGTCAAAT	ATATTTAACT	ATTTAGAGAA	TGATTTCCAC	CTTTATGTT	1440
TAATATCCTA	GGCATCTGCT	GTAATAATAT	TTTAGAAAAT	GTTGGAATT	TAAGAAATAA	1500
CTTGTGTTAC	TAATTTGTAT	AACCCATATC	TGTGCAATGG	AATATAAATA	TCACAAAGTT	1560
GTTTAAAAAA	AAAAAA	AAATTCCCTGC	GGCCGC			1596

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Ala	Trp	Arg	Arg	Glu	Ala	Gly	Val	Gly	Ala	Arg	Gly	Val	Leu	
1			5			10			15						
Ala	Leu	Ala	Leu	Leu	Ala	Leu	Cys	Val	Pro	Gly	Ala	Arg	Gly		
			20			25			30						
Arg	Ala	Leu	Glu	Trp	Phe	Ser	Ala	Val	Val	Asn	Ile	Glu	Tyr	Val	Asp
			35			40			45						
Pro	Gln	Thr	Asn	Leu	Thr	Val	Trp	Ser	Val	Ser	Glu	Ser	Gly	Arg	Phe
			50			55			60						
Gly	Asp	Ser	Ser	Pro	Lys	Glu	Gly	Ala	His	Gly	Leu	Val	Gly	Val	Pro
			65			70			75			80			
Trp	Ala	Pro	Gly	Gly	Asp	Leu	Glu	Gly	Cys	Ala	Pro	Asp	Thr	Arg	Phe
			85			90			95						
Phe	Val	Pro	Glu	Pro	Gly	Gly	Arg	Gly	Ala	Ala	Pro	Trp	Val	Ala	Leu
			100			105			110						
Val	Ala	Arg	Gly	Gly	Cys	Thr	Phe	Lys	Asp	Lys	Val	Leu	Val	Ala	Ala
			115			120			125						
Arg	Arg	Asn	Ala	Ser	Ala	Val	Val	Leu	Tyr	Asn	Glu	Glu	Arg	Tyr	Gly
			130			135			140						
Asn	Ile	Thr	Leu	Pro	Met	Ser	His	Ala	Gly	Thr	Gly	Asn	Ile	Val	Val
			145			150			155			160			
Ile	Met	Ile	Ser	Tyr	Pro	Lys	Gly	Arg	Glu	Ile	Leu	Glu	Leu	Val	Gln

	165	170	175												
Lys	Gly	Ile	Pro	Val	Thr	Met	Thr	Ile	Gly	Val	Gly	Thr	Arg	His	Val
		180						185						190	
Gln	Glu	Phe	Ile	Ser	Gly	Gln	Ser	Val	Val	Phe	Val	Ala	Ile	Ala	Phe
		195						200						205	
Ile	Thr	Met	Met	Ile	Ile	Ser	Leu	Ala	Trp	Leu	Ile	Phe	Tyr	Tyr	Ile
		210			215					220					
Gln	Arg	Phe	Leu	Tyr	Thr	Gly	Ser	Gln	Ile	Gly	Ser	Gln	Ser	His	Arg
		225			230					235				240	
Lys	Glu	Thr	Lys	Lys	Val	Ile	Gly	Gln	Leu	Leu	Leu	His	Thr	Val	Lys
		245					250							255	
His	Gly	Glu	Lys	Gly	Ile	Asp	Val	Asp	Ala	Glu	Asn	Cys	Ala	Val	Cys
		260				265					270				
Ile	Glu	Asn	Phe	Lys	Val	Lys	Asp	Ile	Ile	Arg	Ile	Leu	Pro	Cys	Lys
		275				280					285				
His	Ile	Phe	His	Arg	Ile	Cys	Ile	Asp	Pro	Trp	Leu	Leu	Asp	His	Arg
		290			295					300					
Thr	Cys	Pro	Met	Cys	Lys	Leu	Asp	Val	Ile	Lys	Ala	Leu	Gly	Tyr	Trp
		305			310					315				320	
Gly	Glu	Pro	Gly	Asp	Val	Gln	Glu	Met	Pro	Ala	Pro	Glu	Ser	Pro	Pro
		325				330							335		
Gly	Arg	Asp	Pro	Ala	Ala	Asn	Leu	Ser	Leu	Ala	Leu	Pro	Asp	Asp	Asp
		340				345					350				
Gly	Ser	Asp	Asp	Ser	Ser	Pro	Pro	Ser	Ala	Ser	Pro	Ala	Glu	Ser	Glu
		355				360					365				
Pro	Gln	Cys	Asp	Pro	Ser	Phe	Lys	Gly	Asp	Ala	Gly	Glu	Asn	Thr	Ala
		370			375					380					
Leu	Leu	Glu	Ala	Gly	Arg	Ser	Asp	Ser	Arg	His	Gly	Gly	Pro	Ile	Ser
		385			390					395				400	

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Asp	Lys	Gly	Ser	Ala	Gly	His	Pro	Gly	Gly	Val	Leu	Val	Trp	Gly
					5			10						15	
Arg	Ser	Pro	Ala	Pro	Thr	Ala	Leu	Trp	Gly	Ala	Ser	Pro	Trp	Leu	Ser
					20			25						30	
Pro	Leu	Thr	Ser	Ala	Leu	Arg	Gln	Pro	Leu	His	Arg	Ala	Pro	Leu	Leu
					35			40			45				
Pro	Gly	Gln	Leu	Cys	Trp	Ser	Pro	Arg	Pro	Leu	Glu	Lys	Asn	Lys	Ala
					50			55			60				
Met	Gly	Arg	Pro	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Gln	Pro	Pro		
					65			70			75			80	
Ala	Phe	Leu	Gln	Pro	Gly	Gly	Ser	Thr	Gly	Ser	Gly	Pro	Ser	Tyr	Leu
					85			90			95				
Tyr	Gly	Val	Thr	Gln	Pro	Lys	His	Leu	Ser	Ala	Ser	Met	Gly	Gly	Ser
					100			105			110				
Val	Glu	Ile	Pro	Phe	Ser	Phe	Tyr	Tyr	Pro	Trp	Glu	Leu	Ala	Ile	Val

115	120	125	
Pro Asn Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser			
130	135	140	
Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg			
145	150	155	160
Leu Phe Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu Arg Ile			
165	170	175	
Ser Asn Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg Val Glu			
180	185	190	
Leu Asp Thr Arg Arg Ser Gly Arg Gln Gln Leu Gln Ser Ile Lys Gly			
195	200	205	
Thr Lys Leu Thr Ile Thr Gln Ala Val Thr Thr Thr Thr Trp Arg			
210	215	220	
Pro Ser Ser Thr Thr Ile Ala Gly Leu Arg Val Thr Glu Ser Lys			
225	230	235	240
Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Ile Arg Val			
245	250	255	
Ala Leu Ala Val Ala Val Leu Lys Thr Val Ile Leu Gly Leu Leu Cys			
260	265	270	
Leu Leu Leu Leu Trp Trp Arg Arg Arg Lys Gly Ser Arg Ala Pro Ser			
275	280	285	
Ser Asp Phe			
290			

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Thr Val Ser Gln Arg Phe Gln Leu Ser Asn Ser Gly Pro Asn Ser			
1	5	10	15
Thr Ile Lys Met Lys Ile Ala Leu Arg Val Leu His Leu Glu Lys Arg			
20	25	30	
Glu Arg Pro Pro Asp His Gln His Ser Ala Gln Val Lys Arg Pro Ser			
35	40	45	
Val Ser Lys Glu Gly Arg Lys Thr Ser Ile Lys Ser His Met Ser Gly			
50	55	60	
Ser Pro Gly Pro Gly Gly Ser Asn Thr Ala Pro Ser Thr Pro Val Ile			
65	70	75	80
Gly Gly Ser Asp Lys Pro Gly Met Glu Glu Lys Ala Gln Pro Pro Glu			
85	90	95	
Ala Gly Pro Gln Gly Leu His Asp Leu Gly Arg Ser Ser Ser Ser Leu			
100	105	110	
Leu Ala Ser Pro Gly His Ile Ser Val Lys Glu Pro Thr Pro Ser Ile			
115	120	125	
Ala Ser Asp Ile Ser Leu Pro Ile Ala Thr Gln Glu Leu Arg Gln Arg			
130	135	140	
Leu Arg Gln Leu Glu Asn Gly Thr Thr Leu Gly Gln Ser Pro Leu Gly			
145	150	155	160
Gln Ile Gln Leu Thr Ile Arg His Ser Ser Gln Arg Asn Lys Leu Ile			

165	170	175
Val Val Val His Ala Cys Arg Asn Leu Ile Ala Phe Ser Glu Asp Gly		
180	185	190
Ser Asp Pro Tyr Val Arg Met Tyr Leu Leu Pro Asp Lys Arg Arg Ser		
195	200	205
Gly Arg Arg Lys Thr His Val Ser Lys Lys Thr Leu Asn Pro Val Phe		
210	215	220
Asp Gln Ser Phe Asp Phe Ser Val Ser Leu Pro Glu Val Gln Arg Arg		
225	230	235
Thr Leu Asp Val Ala Val Lys Asn Ser Gly Gly Phe Leu Ser Lys Asp		
245	250	255
Lys Gly Leu Leu Gly Lys Val Leu Val Ala Leu Ala Ser Glu Glu Leu		
260	265	270
Ala Lys Gly Trp Thr Gln Trp Tyr Asp Leu Thr Glu Asp Gly Thr Arg		
275	280	285
Pro Gln Ala Met Thr		
290		

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Glu Arg Arg His Pro Val Cys Ser Gly Thr Cys Gln Pro Thr Gln			
1	5	10	15
Phe Arg Cys Ser Asn Gly Cys Cys Ile Asp Ser Phe Leu Glu Cys Asp			
20	25	30	
Asp Thr Pro Asn Cys Pro Asp Ala Ser Asp Glu Ala Ala Cys Glu Lys			
35	40	45	
Tyr Thr Ser Gly Phe Asp Glu Leu Gln Arg Ile His Phe Pro Ser Asp			
50	55	60	
Lys Gly His Cys Val Asp Leu Pro Asp Thr Gly Leu Cys Lys Glu Ser			
65	70	75	80
Ile Pro Arg Trp Tyr Tyr Asn Pro Phe Ser Glu His Cys Ala Arg Phe			
85	90	95	
Thr Tyr Gly Gly Cys Tyr Gly Asn Lys Asn Asn Phe Glu Glu Gln			
100	105	110	
Gln Cys Leu Glu Ser Cys Arg Gly Ile Ser Lys Lys Asp Val Phe Gly			
115	120	125	
Leu Arg Arg Glu Ile Pro Ile Pro Ser Thr Gly Ser Val Glu Met Ala			
130	135	140	
Val Ala Val Phe Leu Val Ile Cys Ile Val Val Val Ala Ile Leu			
145	150	155	160
Gly Tyr Cys Phe Phe Lys Asn Gln Arg Lys Asp Phe His Gly His His			
165	170	175	
His His Pro Pro Pro Thr Pro Ala Ser Ser Thr Val Ser Thr Thr Glu			
180	185	190	
Asp Thr Glu His Leu Val Tyr Asn His Thr Thr Arg Pro Leu			
195	200	205	

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Ala Gly Leu Ser Arg Gly Ser Ala Arg Ala Leu Leu Ala Ala Leu
 1 5 10 15
 Leu Ala Ser Thr Leu Leu Ala Leu Leu Val Ser Pro Ala Arg Gly Arg
 20 25 30
 Gly Gly Arg Asp His Gly Asp Trp Asp Glu Ala Ser Arg Leu Pro Pro
 35 40 45
 Leu Pro Pro Arg Glu Asp Ala Ala Arg Val Ala Arg Phe Val Thr His
 50 55 60
 Val Ser Asp Trp Gly Ala Leu Ala Thr Ile Ser Thr Leu Glu Ala Val
 65 70 75 80
 Arg Gly Arg Pro Phe Ala Asp Val Leu Ser Leu Ser Asp Gly Pro Pro
 85 90 95
 Gly Ala Gly Ser Gly Val Pro Tyr Phe Tyr Leu Ser Pro Leu Gln Leu
 100 105 110
 Ser Val Ser Asn Leu Gln Glu Asn Pro Tyr Ala Thr Leu Thr Met Thr
 115 120 125
 Leu Ala Gln Thr Asn Phe Cys Lys Lys His Gly Phe Asp Pro Gln Ser
 130 135 140
 Pro Leu Cys Val His Ile Met Leu Ser Gly Thr Val Thr Lys Val Asn
 145 150 155 160
 Glu Thr Glu Met Asp Ile Ala Lys His Ser Leu Phe Ile Arg His Pro
 165 170 175
 Glu Met Lys Thr Trp Pro Ser Ser His Asn Trp Phe Phe Ala Lys Leu
 180 185 190
 Asn Ile Thr Asn Ile Trp Val Leu Asp Tyr Phe Gly Gly Pro Lys Ile
 195 200 205
 Val Thr Pro Glu Glu Tyr Tyr Asn Val Thr Val Gln
 210 215 220

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Asp His His Cys Pro Trp Leu Asn Asn Cys Val Gly His Tyr Asn
 1 5 10 15
 His Arg Tyr Phe Phe Ser Phe Cys Phe Phe Met Thr Leu Gly Cys Val
 20 25 30

Tyr Cys Ser Tyr Gly Ser Trp Asp Leu Phe Arg Glu Ala Tyr Ala Ala
 35 40 45
 Ile Glu Lys Met Lys Gln Leu Asp Lys Asn Lys Leu Gln Ala Val Ala
 50 55 60
 Asn Gln Thr Tyr His Gln Thr Pro Pro Pro Thr Phe Ser Phe Arg Glu
 65 70 75 80
 Arg Met Thr His Lys Ser Leu Val Tyr Leu Trp Phe Leu Cys Ser Ser
 85 90 95
 Val Ala Leu Ala Leu Gly Ala Leu Thr Val Trp His Ala Val Leu Ile
 100 105 110
 Ser Arg Gly Glu Thr Ser Ile Glu Arg His Ile Asn Lys Lys Glu Arg
 115 120 125
 Arg Arg Leu Gln Ala Lys Gly Arg Val Phe Arg Asn Pro Tyr Asn Tyr
 130 135 140
 Gly Cys Leu Asp Asn Trp Lys Val Phe Leu Gly Val Asp Thr Gly Arg
 145 150 155 160
 His Trp Leu Thr Arg Val Leu Leu Pro Ser Thr His Leu Pro His Gly
 165 170 175
 Asn Gly Met Ser Trp Glu Pro Pro Trp Val Thr Ala His Ser Ala
 180 185 190
 Ser Val Met Ala Val
 195

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ala Pro Leu Gly Met Leu Leu Gly Leu Leu Met Ala Ala Cys Phe
 1 5 10 15
 Thr Phe Cys Leu Ser His Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn
 20 25 30
 Pro Glu Lys Ser Ser Thr Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala
 35 40 45
 Glu Glu Glu Leu Asp Ala Glu Val Leu Glu Val Phe His Pro Thr His
 50 55 60
 Glu Trp Gln Ala Leu Gln Pro Gly Gln Ala Val Pro Ala Gly Ser His
 65 70 75 80
 Val Arg Leu Asn Leu Gln Thr Gly Glu Arg Glu Ala Lys Leu Gln Tyr
 85 90 95
 Glu Asp Lys Phe Arg Asn Asn Leu Lys Gly Lys Arg Leu Asp Ile Asn
 100 105 110
 Thr Asn Thr Tyr Thr Ser Gln Asp Leu Lys Ser Ala Leu Ala Lys Phe
 115 120 125
 Lys Glu Gly Ala Glu Met Glu Ser Ser Lys Glu Asp Lys Ala Arg Gln
 130 135 140
 Ala Glu Val Lys Arg Leu Phe Arg Pro Ile Glu Glu Leu Lys Lys Asp
 145 150 155 160
 Phe Asp Glu Leu Asn Val Val Ile Glu Thr Asp Met Gln Ile Met Val
 165 170 175

Arg Leu Ile Asn Lys Phe Asn Ser Ser Ser Ser Leu Glu Glu Lys
 180 185 190
 Ile Ala Ala Leu Phe Asp Leu Glu Tyr Tyr Val His Gln Met Asp Asn
 195 200 205
 Ala Gln Asp Leu Leu Ser Phe Gly Gly Leu Gln Val Val Ile Asn Gly
 210 215 220
 Leu Asn Ser Thr Glu Pro Leu Val Lys Glu Tyr Ala Ala Phe Val Leu
 225 230 235 240
 Gly Ala Ala Phe Ser Ser Asn Pro Lys Val Gln Val Glu Ala Ile Glu
 245 250 255
 Gly Gly Ala Leu Gln Lys Leu Leu Val Ile Leu Ala Thr Glu Gln Pro
 260 265 270
 Leu Thr Ala Lys Lys Val Leu Phe Ala Leu Cys Ser Leu Leu Arg
 275 280 285
 His Phe Pro Tyr Ala Gln Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln
 290 295 300
 Val Leu Arg Thr Leu Val Gln Glu Lys Gly Thr Glu Val Leu Ala Val
 305 310 315 320
 Arg Val Val Thr Leu Leu Tyr Asp Leu Val Thr Glu Lys Met Phe Ala
 325 330 335
 Glu Glu Glu Ala Glu Leu Thr Gln Glu Met Ser Pro Glu Lys Leu Gln
 340 345 350
 Gln Tyr Arg Gln Val His Leu Leu Pro Gly Leu Trp Glu Gln Gly Trp
 355 360 365
 Cys Glu Ile Thr Ala His Leu Leu Ala Leu Pro Glu His Asp Ala Arg
 370 375 380
 Glu Lys Val Leu Gln Thr Leu Gly Val Leu Leu Thr Thr Cys Arg Asp
 385 390 395 400
 Arg Tyr Arg Gln Asp Pro Gln Leu Gly Arg Thr Leu Ala Ser Leu Gln
 405 410 415
 Ala Glu Tyr Gln Val Leu Ala Ser Leu Glu Leu Gln Asp Gly Glu Asp
 420 425 430
 Glu Gly Tyr Phe Gln Glu Leu Leu Gly Ser Val Asn Ser Leu Leu Lys
 435 440 445
 Glu Leu Arg
 450

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Trp Gln Ala Gly Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr
 1 5 10 15
 Ala Asn Ile Asp Ile Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln
 20 25 30
 Val Arg Ser Arg Leu Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn
 35 40 45
 Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr Gly Pro Leu Met Leu Val
 50 55 60

Phe Thr Leu Val Ala Ile Leu Leu His Gly Met Lys Thr Ser Asp Thr
 65 70 75 80
 Ile Ile Arg Glu Gly Thr Leu Met Gly Thr Ala Ile Gly Thr Cys Phe
 85 90 95
 Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile Tyr Phe Leu Ala Tyr Leu
 100 105 110
 Cys Asn Ala Gln Ile Thr Met Leu Gln Met Leu Ala Leu Leu Gly Tyr
 115 120 125
 Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr Tyr Asn Ile His
 130 135 140
 Leu His Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val Gly Gly Leu Ser
 145 150 155 160
 Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr Val Gly Pro Thr
 165 170 175
 Gln Arg Leu Leu Cys Gly Thr Leu Ala Ala Leu His Met Leu Phe
 180 185 190
 Leu Leu Tyr Leu His Phe Ala Tyr His Lys Val Val Glu Gly Ile Leu
 195 200 205
 Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln Arg Val Pro Arg
 210 215 220
 Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro Thr Thr Val Leu
 225 230 235 240
 Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln Ser His
 245 250

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Gly Ser Glu Asn Glu Ala Leu Asp Leu Ser Met Lys Ser Val Pro
 1 5 10 15
 Trp Leu Lys Ala Gly Glu Val Ser Pro Pro Ile Phe Gln Glu Asp Ala
 20 25 30
 Ala Leu Asp Leu Ser Val Ala Ala His Arg Lys Ser Glu Pro Pro Pro
 35 40 45
 Glu Thr Leu Tyr Asp Ser Gly Ala Ser Val Asp Ser Ser Gly His Thr
 50 55 60
 Val Met Glu Lys Leu Pro Ser Gly Met Glu Ile Ser Phe Ala Pro Ala
 65 70 75 80
 Thr Ser His Glu Ala Pro Ala Met Met Asp Ser His Ile Ser Ser Ser
 85 90 95
 Asp Ala Ala Thr Glu Met Leu Ser Gln Pro Asn His Pro Ser Gly Glu
 100 105 110
 Val Lys Ala Glu Asn Asn Ile Glu Met Val Gly Glu Ser Gln Ala Ala
 115 120 125
 Lys Val Ile Val Ser Val Glu Asp Ala Val Pro Thr Ile Phe Cys Gly
 130 135 140
 Lys Ile Lys Gly Leu Ser Gly Val Ser Thr Lys Asn Phe Ser Phe Lys
 145 150 155 160

Arg	Glu	Asp	Ser	Val	Leu	Gln	Gly	Tyr	Asp	Ile	Asn	Ser	Gln	Gly	Glu
															175
															165
															170
Glu	Ser	Met	Gly	Asn	Ala	Glu	Pro	Leu	Arg	Lys	Pro	Ile	Lys	Asn	Arg
															190
															180
															185
Ser	Ile	Lys	Leu	Lys	Lys	Val	Asn	Ser	Gln	Glu	Val	His	Met	Leu	Pro
															205
															195
															200
Ile	Lys	Lys	Gln	Arg	Leu	Ala	Thr	Phe	Phe	Pro	Arg	Lys			
															220
															210
															215

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Val	Lys	Val	Thr	Phe	Asn	Ser	Ala	Leu	Ala	Gln	Glu	Ala	Lys	
1														15	
														10	
Lys	Asp	Glu	Pro	Lys	Ser	Gly	Glu	Glu	Ala	Leu	Ile	Ile	Pro	Pro	Asp
															30
															20
Ala	Val	Ala	Val	Asp	Cys	Lys	Asp	Pro	Asp	Asp	Val	Val	Pro	Val	Gly
															45
															35
Gln	Arg	Arg	Ala	Trp	Cys	Trp	Cys	Met	Cys	Phe	Gly	Leu	Ala	Phe	Met
															50
															55
Leu	Ala	Gly	Val	Ile	Leu	Gly	Gly	Ala	Tyr	Leu	Tyr	Lys	Tyr	Phe	Ala
															80
															65
Leu	Gln	Pro	Asp	Asp	Val	Tyr	Tyr	Cys	Gly	Ile	Lys	Tyr	Ile	Lys	Asp
															95
															85
Asp	Val	Ile	Leu	Asn	Glu	Pro	Ser	Ala	Asp	Ala	Pro	Ala	Ala	Leu	Tyr
															100
															105
Gln	Thr	Ile	Glu	Glu	Asn	Ile	Lys	Ile	Phe	Glu	Glu	Glu	Val	Glu	
															115
															120
Phe	Ile	Ser	Val	Pro	Val	Pro	Glu	Phe	Ala	Asp	Ser	Asp	Pro	Ala	Asn
															130
															135
Ile	Val	His	Asp	Phe	Asn	Lys	Lys	Leu	Thr	Ala	Tyr	Leu	Asp	Leu	Asn
															145
															150
Leu	Asp	Lys	Cys	Tyr	Val	Ile	Pro	Leu	Asn	Thr	Ser	Ile	Val	Met	Pro
															165
															170
Pro	Arg	Asn	Leu	Leu	Glu	Leu	Leu	Ile	Asn	Ile	Lys	Ala	Gly	Thr	Tyr
															180
															185
Leu	Pro	Gln	Ser	Tyr	Leu	Ile	His	Glu	His	Met	Val	Ile	Thr	Asp	Arg
															195
															200
Ile	Glu	Asn	Ile	Asp	His	Leu	Gly	Phe	Phe	Ile	Tyr	Arg	Leu	Cys	His
															210
															215
Asp	Lys	Glu	Thr	Tyr	Lys	Leu	Gln	Arg	Arg	Glu	Thr	Ile	Lys	Gly	Ile
															225
															230
Gln	Lys	Arg	Glu	Ala	Ser	Asn	Cys	Phe	Ala	Ile	Arg	His	Phe	Glu	Asn
															245
															250
Lys	Phe	Ala	Val	Glu	Thr	Leu	Ile	Cys	Ser						
															260
															265

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met	Pro	Thr	Gly	Asp	Phe	Asp	Ser	Lys	Pro	Ser	Trp	Ala	Asp	Gln	Val
1			5					10						15	
Glu	Glu	Glu	Gly	Glu	Asp	Asp	Lys	Cys	Val	Thr	Ser	Glu	Leu	Leu	Lys
								20		25				30	
Gly	Ile	Pro	Leu	Ala	Thr	Gly	Asp	Thr	Ser	Pro	Glu	Pro	Glu	Leu	Leu
								35		40				45	
Pro	Gly	Ala	Pro	Leu	Pro	Pro	Pro	Lys	Glu	Val	Ile	Asn	Gly	Asn	Ile
	50							55					60		
Lys	Thr	Val	Thr	Glu	Tyr	Lys	Ile	Asp	Glu	Asp	Gly	Lys	Lys	Phe	Lys
	65						70				75			80	
Ile	Val	Arg	Thr	Phe	Arg	Ile	Glu	Thr	Arg	Lys	Ala	Ser	Lys	Ala	Val
								85		90				95	
Ala	Arg	Arg	Lys	Asn	Trp	Lys	Lys	Phe	Gly	Asn	Ser	Glu	Phe	Asp	Pro
							100		105				110		
Pro	Gly	Pro	Asn	Val	Ala	Thr	Thr	Val	Ser	Asp	Asp	Val	Ser	Met	
							115		120				125		
Thr	Phe	Ile	Thr	Ser	Lys	Glu	Asp	Leu	Asn	Cys	Gln	Glu	Glu	Asp	
	130					135					140				
Pro	Met	Asn	Lys	Phe	Lys	Gly	Gln	Lys	Ile	Val	Ser	Cys	Arg	Ile	Cys
	145					150				155			160		
Lys	Gly	Asp	His	Trp	Thr	Thr	Arg	Cys	Pro	Tyr	Lys	Asp	Thr	Leu	Gly
							165			170			175		
Pro	Met	Gln	Lys	Glu	Leu	Ala	Glu	Gln	Leu	Gly	Leu	Ser	Thr	Gly	Glu
							180		185				190		
Lys	Glu	Lys	Leu	Pro	Gly	Glu	Leu	Glu	Pro	Val	Gln	Ala	Thr	Gln	Asn
							195		200				205		
Lys	Thr	Gly	Lys	Tyr	Val	Pro	Pro	Ser	Leu	Arg	Asp	Gly	Ala	Ser	Arg
							210		215				220		
Arg	Gly	Glu	Ser	Met	Gln	Pro	Asn	Arg	Arg	Ala	Asp	Asp	Asn	Ala	Thr
	225							230		235				240	
Ile	Arg	Val	Thr	Asn	Leu	Arg	Arg	Gly	His	Ala					
					245			250							

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Arg Arg Leu Asn Arg Lys Lys Thr Leu Ser Leu Val Lys Glu Leu

1	5	10	15												
Asp	Ala	Phe	Pro	Lys	Val	Pro	Glu	Ser	Tyr	Val	Glu	Thr	Ser	Ala	Ser
															30
20															
Gly	Gly	Thr	Val	Ser	Leu	Ile	Ala	Phe	Thr	Thr	Met	Ala	Leu	Leu	Thr
															45
35															
Ile	Met	Glu	Phe	Ser	Val	Tyr	Gln	Asp	Thr	Trp	Met	Lys	Tyr	Glu	Tyr
															60
50															
Glu	Val	Asp	Lys	Asp	Phe	Ser	Ser	Lys	Leu	Arg	Ile	Asn	Ile	Asp	Ile
															80
65															
70															
Thr	Val	Ala	Met	Lys	Cys	Gln	Tyr	Val	Gly	Ala	Asp	Val	Leu	Asp	Leu
															95
85															
Ala	Glu	Thr	Met	Val	Ala	Ser	Ala	Asp	Gly	Leu	Val	Tyr	Glu	Pro	Thr
															110
100															
Val	Phe	Asp	Leu	Ser	Pro	Gln	Gln	Lys	Glu	Trp	Gln	Arg	Met	Leu	Gln
															125
115															
Leu	Ile	Gln	Ser	Arg	Leu	Gln	Glu	Glu	His	Ser	Leu	Gln	Asp	Val	Ile
															140
130															
Phe	Lys	Ser	Ala	Phe	Lys	Ser	Thr	Ser	Thr	Ala	Leu	Pro	Pro	Arg	Glu
															160
145															
150															
Asp	Asp	Ser	Ser	Gln	Ser	Pro	Asn	Ala	Cys	Arg	Ile	His	Gly	His	Leu
															175
165															
Tyr	Val	Asn	Lys	Val	Ala	Gly	Asn	Phe	His	Ile	Thr	Val	Gly	Lys	Ala
															190
180															
Ile	Pro	His	Pro	Arg	Gly	His	Ala	His	Leu	Ala	Ala	Leu	Val	Asn	His
															205
195															
Glu	Ser	Tyr	Asn	Phe	Ser	His	Arg	Ile	Asp	His	Leu	Ser	Phe	Gly	Glu
															220
210															
Leu	Val	Pro	Ala	Ile	Ile	Asn	Pro	Leu	Asp	Gly	Thr	Glu	Lys	Ile	Ala
															240
225															
230															
Ile	Asp	His	Asn	Gln	Met	Phe	Gln	Tyr	Phe	Ile	Thr	Val	Val	Pro	Thr
															255
245															
Lys	Leu	His	Thr	Tyr	Lys	Ile	Ser	Ala	Asp	Thr	His	Gln	Phe	Ser	Val
															270
260															
Thr	Glu	Arg	Glu	Arg	Ile	Ile	Asn	His	Ala	Ala	Gly	Ser	His	Gly	Val
															285
275															
Ser	Gly	Ile	Phe	Met	Lys	Tyr	Asp	Leu	Ser	Ser	Leu	Met	Val	Thr	Val
															300
290															
Thr	Glu	Glu	His	Met	Pro	Phe	Trp	Gln	Phe	Phe	Val	Arg	Leu	Cys	Gly
															320
305															
310															
Ile	Val	Gly	Gly	Ile	Phe	Ser	Thr	Thr	Gly	Met	Leu	His	Gly	Ile	Gly
															335
325															
Lys	Phe	Ile	Val	Glu	Ile	Cys	Cys	Arg	Phe	Arg	Leu	Gly	Ser	Tyr	
															350
340															
Lys	Pro	Val	Asn	Ser	Val	Pro	Phe	Glu	Asp	Gly	His	Thr	Asp	Asn	His
															365
355															
Leu	Pro	Leu	Leu	Glu	Asn	Asn	Thr	His							
370															
375															

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Gly Ser Gln His Ser Ala Ala Ala Arg Pro Ser Ser Cys Arg Arg
 1 5 10 15
 Lys Gln Glu Asp Asp Arg Asp Gly Leu Leu Ala Glu Arg Glu Gln Glu
 20 25 30
 Glu Ala Ile Ala Gln Phe Pro Tyr Val Glu Phe Thr Gly Arg Asp Ser
 35 40 45
 Ile Thr Cys Leu Thr Cys Gln Gly Thr Gly Tyr Ile Pro Thr Glu Gln
 50 55 60
 Val Asn Glu Leu Val Ala Leu Ile Pro His Ser Asp Gln Arg Leu Arg
 65 70 75 80
 Pro Gln Arg Thr Lys Gln Tyr Val Leu Leu Ser Ile Leu Leu Cys Leu
 85 90 95
 Leu Ala Ser Gly Leu Val Val Phe Phe Leu Phe Pro His Ser Val Leu
 100 105 110
 Val Asp Asp Asp Gly Ile Lys Val Val Lys Val Thr Phe Asn Lys Gln
 115 120 125
 Asp Ser Leu Val Ile Leu Thr Ile Met Ala Thr Leu Lys Ile Arg Asn
 130 135 140
 Ser Asn Phe Tyr Thr Val Ala Val Thr Ser Leu Ser Ser Gln Ile Gln
 145 150 155 160
 Tyr Met Asn Thr Val Val Ser Thr Tyr Val Thr Thr Asn Val Ser Leu
 165 170 175
 Ile Pro Pro Arg Ser Glu Gln Leu Val Asn Phe Thr Gly Lys Ala Glu
 180 185 190
 Met Gly Gly Pro Phe Ser Tyr Val Tyr Phe Phe Cys Thr Val Pro Glu
 195 200 205
 Ile Leu Val His Asn Ile Val Ile Phe Met Arg Thr Ser Val Lys Ile
 210 215 220
 Ser Tyr Ile Gly Leu Met Thr Gln Ser Ser Leu Glu Thr His His Tyr
 225 230 235 240
 Val Asp Cys Gly Gly Asn Ser Thr Ala Ile
 245 250

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Val Thr Cys Phe His Val Pro Tyr Ser Ala Leu Thr Met Phe Ile
 1 5 10 15
 Ser Thr Glu Gln Thr Glu Arg Asp Ser Ala Thr Ala Tyr Arg Met Thr
 20 25 30
 Val Glu Val Leu Gly Thr Val Leu Gly Thr Ala Ile Gln Gly Gln Ile
 35 40 45
 Val Gly Gln Ala Asp Thr Pro Cys Phe Gln Asp Leu Asn Ser Ser Thr
 50 55 60
 Val Ala Ser Gln Ser Ala Asn His Thr His Gly Thr Thr Ser His Arg

65	70	75	80												
Glu	Thr	Gln	Lys	Ala	Tyr	Leu	Leu	Ala	Ala	Gly	Val	Ile	Val	Cys	Ile
85														95	
Tyr	Ile	Ile	Cys	Ala	Val	Ile	Leu	Ile	Leu	Gly	Val	Arg	Glu	Gln	Arg
100														110	
Glu	Pro	Tyr	Glu	Ala	Gln	Gln	Ser	Glu	Pro	Ile	Ala	Tyr	Phe	Arg	Gly
115														125	
Leu	Arg	Leu	Val	Met	Ser	His	Gly	Pro	Tyr	Ile	Lys	Leu	Ile	Thr	Gly
130														140	
Phe	Leu	Phe	Thr	Ser	Leu	Ala	Phe	Met	Leu	Val	Glu	Gly	Asn	Phe	Val
145														160	
Leu	Phe	Cys	Thr	Tyr	Thr	Leu	Gly	Phe	Arg	Asn	Glu	Phe	Gln	Asn	Leu
165														175	
Leu	Leu	Ala	Ile	Met	Leu	Ser	Ala	Thr	Leu	Thr	Ile	Pro	Ile	Trp	Gln
180														190	
Trp	Phe	Leu	Thr	Arg	Phe	Gly	Lys	Lys	Thr	Ala	Val	Tyr	Val	Gly	Ile
195														205	
Ser	Ser	Ala	Val	Pro	Phe	Leu	Ile	Leu	Val	Ala	Leu	Met	Glu	Ser	Asn
210														220	
Leu	Ile	Ile	Thr	Tyr	Ala	Val	Ala	Val	Ala	Ala	Gly	Ile	Ser	Val	Ala
225														240	
Ala	Ala	Phe	Leu	Leu	Pro	Trp	Ser	Met	Leu	Pro	Asp	Val	Ile	Asp	Asp
245														255	
Phe	His	Leu	Lys	Gln	Pro	His	Phe	His	Gly	Thr	Glu	Pro	Ile	Phe	Phe
260														270	
Ser	Phe	Tyr	Val	Phe	Phe	Thr	Lys	Phe	Ala	Ser	Gly	Val	Ser	Leu	Gly
275														285	
Ile	Ser	Thr	Leu	Ser	Leu	Asp	Phe	Ala	Gly	Tyr	Gln	Thr	Arg	Gly	Cys
290														300	
Ser	Gln	Pro	Glu	Arg	Val	Lys	Phe	Thr	Leu	Asn	Met	Leu	Val	Thr	Met
305														320	
Ala	Pro	Ile	Val	Leu	Ile	Leu	Leu	Gly	Leu	Leu	Leu	Phe	Lys	Met	Tyr
325														335	
Pro	Ile	Asp	Glu	Glu	Arg	Arg	Gln	Asn	Lys	Lys	Ala	Leu	Gln	Ala	
340														350	
Leu	Arg	Asp	Glu	Ala	Ser	Ser	Ser	Gly	Cys	Ser	Glu	Thr	Asp	Ser	Thr
355														365	
Glu	Leu	Ala	Ser	Ile	Leu										
370															

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met	Val	Asn	Asp	Pro	Pro	Val	Pro	Ala	Leu	Leu	Trp	Ala	Gln	Glu	Val
1															15
Gly	Gln	Val	Leu	Ala	Gly	Arg	Ala	Arg	Arg	Leu	Leu	Leu	Gln	Phe	Gly
20														30	
Val	Leu	Phe	Cys	Thr	Ile	Leu	Leu	Leu	Leu	Trp	Val	Ser	Val	Phe	Leu

35	40	45														
Tyr	Gly	Ser	Phe	Tyr	Tyr	Ser	Tyr	Met	Pro	Thr	Val	Ser	His	Leu	Ser	
50				55				60								
Pro	Val	His	Phe	Tyr	Tyr	Arg	Thr	Asp	Cys	Asp	Ser	Ser	Thr	Thr	Ser	
65				70				75							80	
Leu	Cys	Ser	Phe	Pro	Val	Ala	Asn	Val	Ser	Leu	Thr	Lys	Gly	Gly	Arg	
								85				90			95	
Asp	Arg	Val	Leu	Met	Tyr	Gly	Gln	Pro	Tyr	Arg	Val	Thr	Leu	Glu	Leu	
								100			105			110		
Glu	Leu	Pro	Glu	Ser	Pro	Val	Asn	Gln	Asp	Leu	Gly	Met	Phe	Leu	Val	
								115			120			125		
Thr	Ile	Ser	Cys	Tyr	Thr	Arg	Gly	Gly	Arg	Ile	Ile	Ser	Thr	Ser	Ser	
								130			135			140		
Arg	Ser	Val	Met	Leu	His	Tyr	Arg	Ser	Asp	Leu	Leu	Gln	Met	Leu	Asp	
145								150				155			160	
Thr	Leu	Val	Phe	Ser	Ser	Leu	Leu	Leu	Phe	Gly	Phe	Ala	Glu	Gln	Lys	
								165			170			175		
Gln	Leu	Leu	Glu	Val	Glu	Leu	Tyr	Ala	Asp	Tyr	Arg	Glu	Asn	Ser	Tyr	
								180			185			190		
Val	Pro	Thr	Thr	Gly	Ala	Ile	Ile	Glu	Ile	His	Ser	Lys	Arg	Ile	Gln	
								195			200			205		
Leu	Tyr	Gly	Ala	Tyr	Leu	Arg	Ile	His	Ala	His	Phe	Thr	Gly	Leu	Arg	
								210			215			220		
Tyr	Leu	Leu	Tyr	Asn	Phe	Pro	Met	Thr	Cys	Ala	Phe	Ile	Gly	Val	Ala	
								225			230			235		240
Ser	Asn	Phe	Thr	Phe	Leu	Ser	Val	Ile	Val	Leu	Phe	Ser	Tyr	Met	Gln	
								245			250			255		
Trp	Val	Trp	Gly	Gly	Ile	Trp	Pro	Arg	His	Arg	Phe	Ser	Leu	Gln	Val	
								260			265			270		
Asn	Ile	Arg	Lys	Arg	Asp	Asn	Ser	Arg	Lys	Glu	Val	Gln	Arg	Arg	Ile	
								275			280			285		
Ser	Ala	His	Gln	Pro	Gly	Pro	Glu	Gly	Gln	Glu	Glu	Ser	Thr	Pro	Gln	
								290			295			300		
Ser	Asp	Val	Thr	Glu	Asp	Gly	Glu	Ser	Pro	Glu	Asp	Pro	Ser	Gly	Thr	
								305			310			315		320
Glu	Val	Ser	Cys	Pro	Arg	Arg	Arg	Asn	Gln	Ile	Ser	Ser	Pro			
								325			330					

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met	Thr	His	Pro	Gly	Thr	Gly	Asp	Ile	Ile	Ala	Val	Met	Ile	Thr	Glu
1				5				10				15			
Leu	Arg	Gly	Lys	Asp	Ile	Leu	Ser	Tyr	Leu	Glu	Lys	Asn	Ile	Ser	Val
								20			25			30	
Gln	Met	Thr	Ile	Ala	Val	Gly	Thr	Arg	Met	Pro	Pro	Lys	Asn	Phe	Ser
								35			40			45	
Arg	Gly	Ser	Leu	Val	Phe	Val	Ser	Ile	Ser	Phe	Ile	Val	Leu	Met	Ile

50	55	60	
Ile Ser Ser Ala Trp Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg Tyr			
65	70	75	80
Thr Asn Ala Arg Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala Lys			
85	90	95	
Lys Ala Ile Ser Lys Leu Thr Thr Arg Thr Val Lys Lys Gly Asp Lys			
100	105	110	
Glu Thr Asp Pro Asp Phe Asp His Cys Ala Val Cys Ile Glu Ser Tyr			
115	120	125	
Lys Gln Asn Asp Val Val Arg Ile Leu Pro Cys Lys His Val Phe His			
130	135	140	
Lys Ser Cys Val Asp Pro Trp Leu Ser Glu His Cys Thr Cys Pro Met			
145	150	155	160
Cys Lys Leu Asn Ile Leu Lys Ala Leu Gly Ile Val Pro Asn Leu Pro			
165	170	175	
Cys Thr Asp Asn Val Ala Phe Asp Met Glu Arg Leu Thr Arg Thr Gln			
180	185	190	
Ala Val Asn Arg Arg Ser Ala Leu Gly Asp Leu Ala Gly Asp Asn Ser			
195	200	205	
Leu Gly Leu Glu Pro Leu Arg Thr Ser Gly Ile Ser Pro Leu Pro Gln			
210	215	220	
Asp Gly Glu Leu Thr Pro Arg Thr Gly Glu Ile Asn Ile Ala Val Thr			
225	230	235	240
Lys Glu Trp Phe Ile Ile Ala Ser Phe Gly Leu Leu Ser Ala Leu Thr			
245	250	255	
Leu Cys Tyr Met Ile Ile Arg Ala Thr Ala Ser Leu Asn Ala Asn Glu			
260	265	270	
Val Glu Trp Phe			
275			

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 210 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Ala Asn Ser Gly Leu Gln Leu Leu Gly Phe Ser Met Ala Leu Leu			
1	5	10	15
Gly Trp Val Gly Leu Val Ala Cys Thr Ala Ile Pro Gln Trp Gln Met			
20	25	30	
Ser Ser Tyr Ala Gly Asp Asn Ile Ile Thr Ala Gln Ala Met Tyr Lys			
35	40	45	
Gly Leu Trp Met Asp Cys Val Thr Gln Ser Thr Gly Met Met Ser Cys			
50	55	60	
Lys Met Tyr Asp Ser Val Leu Ala Leu Ser Ala Ala Leu Gln Ala Thr			
65	70	75	80
Arg Ala Leu Met Val Val Ser Leu Val Leu Gly Phe Leu Ala Met Phe			
85	90	95	
Val Ala Thr Met Gly Met Lys Cys Thr Arg Cys Gly Gly Asp Asp Lys			
100	105	110	
Val Lys Lys Ala Arg Ile Ala Met Gly Gly Ile Ile Phe Ile Val			

115	120	125													
Ala	Gly	Leu	Ala	Ala	Leu	Val	Ala	Cys	Ser	Trp	Tyr	Gly	His	Gln	Ile
130							135					140			
Val	Thr	Asp	Phe	Tyr	Asn	Pro	Leu	Ile	Pro	Thr	Asn	Ile	Lys	Tyr	Glu
145											155			160	
Phe	Gly	Pro	Ala	Ile	Phe	Ile	Gly	Trp	Ala	Gly	Ser	Ala	Leu	Val	Ile
											170			175	
Leu	Gly	Gly	Ala	Leu	Leu	Ser	Cys	Ser	Cys	Pro	Gly	Asn	Glu	Ser	Lys
											185			190	
Ala	Gly	Tyr	Arg	Ala	Pro	Arg	Ser	Tyr	Pro	Lys	Ser	Asn	Ser	Ser	Lys
											200			205	
Glu	Tyr														
															210

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met	Ile	Arg	Pro	Gln	Leu	Arg	Thr	Ala	Gly	Leu	Gly	Arg	Cys	Leu	Leu
1															15
Pro	Gly	Leu	Leu	Leu	Leu	Val	Pro	Val	Leu	Trp	Ala	Gly	Ala	Glu	
Lys	Leu	His	Thr	Gln	Pro	Ser	Cys	Pro	Ala	Val	Cys	Gln	Pro	Thr	Arg
35															45
Cys	Pro	Ala	Leu	Pro	Thr	Cys	Ala	Leu	Gly	Thr	Thr	Pro	Val	Phe	Asp
50															60
Leu	Cys	Arg	Cys	Cys	Arg	Val	Cys	Pro	Ala	Ala	Glu	Arg	Glu	Val	Cys
65															80
Gly	Gly	Ala	Gln	Gly	Gln	Pro	Cys	Ala	Pro	Gly	Leu	Gln	Cys	Leu	Gln
85															95
Pro	Leu	Arg	Pro	Gly	Phe	Pro	Ser	Thr	Cys	Gly	Cys	Pro	Thr	Leu	Gly
100															110
Gly	Ala	Val	Cys	Gly	Ser	Asp	Arg	Arg	Thr	Tyr	Pro	Ser	Met	Cys	Ala
115															125
Leu	Arg	Ala	Glu	Asn	Arg	Ala	Ala	Arg	Arg	Leu	Gly	Lys	Val	Pro	Ala
130															140
Val	Pro	Val	Gln	Trp	Gly	Asn	Cys	Gly	Asp	Thr	Gly	Thr	Arg	Ser	Ala
145															160
Gly	Pro	Leu	Arg	Arg	Asn	Tyr	Asn	Phe	Ile	Ala	Ala	Val	Val	Glu	Lys
165															175
Val	Ala	Pro	Ser	Val	Val	His	Val	Gln	Leu	Trp	Gly	Arg	Leu	Leu	His
180															190
Gly	Ser	Arg	Leu	Val	Pro	Val	Tyr	Ser	Gly	Ser	Gly	Phe	Ile	Val	Ser
195															205
Glu	Asp	Gly	Leu	Ile	Ile	Thr	Asn	Ala	His	Val	Val	Arg	Asn	Gln	Gln
210															220
Trp	Ile	Glu	Val	Val	Leu	Gln	Asn	Gly	Ala	Arg	Tyr	Glu	Ala	Val	Val
225															240
Lys	Asp	Ile	Asp	Leu	Lys	Leu	Asp	Leu	Ala	Val	Ile	Lys	Ile	Glu	Ser

245	250	255
Asn Ala Glu Leu Pro Val Leu Met Leu Gly Arg Ser Ser Asp	Leu Arg	
260	265	270
Ala Gly Glu Phe Val Val Ala Leu Gly Ser Pro Phe Ser	Leu Gln Asn	
275	280	285
Thr Ala Thr Ala Gly Ile Val Ser Thr Lys Gln Arg Gly	Gly Lys Glu	
290	295	300
Leu Gly Met Lys Asp Ser Asp Met Asp Tyr Val Gln Ile	Asp Ala Thr	
305	310	315
Ile Asn Tyr Gly Asn Ser Gly Gly Pro Leu Val Asn Leu	Asp Gly Asp	
325	330	335
Val Ile Gly Val Asn Ser Leu Arg Val Thr Asp Gly Ile	Ser Phe Ala	
340	345	350
Ile Pro Ser Asp Arg Val Arg Gln Phe Leu Ala Glu	Tyr His Glu His	
355	360	365
Gln Met Lys Gly Lys Ala Phe Ser Asn Lys Lys Tyr	Leu Gly Leu Gln	
370	375	380
Met Leu Ser Leu Thr Val Pro Leu Ser Glu Glu Leu Lys	Met His Tyr	
385	390	395
Pro Asp Phe Pro Asp Val Ser Ser Gly Val Tyr Val Cys	Lys Val Val	
405	410	415
Glu Gly Thr Ala Ala Gln Ser Ser Gly Leu Arg Asp His	Asp Val Ile	
420	425	430
Val Asn Ile Asn Gly Lys Pro Ile Thr Thr Thr Asp Val	Val Lys	
435	440	445
Ala Leu Asp Ser Asp Ser Leu Ser Met Ala Val Leu Arg	Gly Lys Asp	
450	455	460
Asn Leu Leu Leu Thr Val Ile Pro Glu Thr Ile Asn		
465	470	475

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Val Lys Val Thr Phe Asn Ser Ala Leu Ala Gln Lys	Glu Ala Lys		
1	5	10	15
Lys Asp Glu Pro Glu Ser Gly Glu Glu Ala Leu Ile Ile	Pro Pro Asp		
20	25	30	
Ala Val Ala Val Asp Cys Lys Asp Pro Asp Asp Val Val	Pro Val Gly		
35	40	45	
Gln Arg Arg Ala Trp Cys Trp Cys Met Cys Phe Gly	Leu Ala Phe Met		
50	55	60	
Leu Ala Gly Val Ile Leu Gly Gly Ala Tyr Leu Tyr Lys	Tyr Phe Ala		
65	70	75	80
Leu Gln Pro Asp Asp Val Tyr Tyr Cys Gly Ile Lys Tyr	Ile Lys Asp		
85	90	95	
Asp Val Ile Leu Asn Glu Pro Ser Ala Asp Ala Pro Ala	Leu Tyr		
100	105	110	
Gln Thr Ile Glu Glu Asn Ile Lys Ile Phe Glu Glu Glu	Val Glu		

115	120	125
Phe Ile Ser Val Pro Val Pro Glu Phe Ala Asp Ser Asp Pro Ala Asn		
130	135	140
Ile Val His Asp Phe Asn Lys Lys Leu Thr Ala Tyr Leu Asp Leu Asn		
145	150	155
Leu Asp Lys Cys Tyr Val Ile Pro Leu Asn Thr Ser Ile Val Met Pro		160
165	170	175
Pro Arg Asn Leu Leu Glu Leu Leu Ile Asn Ile Lys Ala Gly Thr Tyr		
180	185	190
Leu Pro Gln Ser Tyr Leu Ile His Glu His Met Val Ile Thr Asp Arg		
195	200	205
Ile Glu Asn Ile Asp His Leu Gly Phe Phe Ile Tyr Arg Leu Cys His		
210	215	220
Asp Lys Glu Thr Tyr Lys Leu Gln Arg Arg Glu Thr Ile Lys Gly Ile		
225	230	235
Gln Lys Arg Glu Ala Ser Asn Cys Phe Ala Ile Arg His Phe Glu Asn		240
245	250	255
Lys Phe Ala Val Glu Thr Leu Ile Cys Ser		
260	265	